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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:00 ; Search time 122.151 Seconds  
(without alignments)  
804.673 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 274  
Sequence: 1 GSHSLRYSTAVSRGRGEP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	274	100.0	274	4	AAG64618	Aag64618 Human can
2	274	100.0	274	7	ADP55588	Adp55588 Fragment
3	274	100.0	362	4	AAG64617	Aag64617 Human can
4	274	100.0	362	4	ABP50296	Abp50296 HLA-Cw ov
5	274	100.0	362	7	ADP55587	Adp55587 Human can
6	274	100.0	362	8	ADJ75372	Adj75372 Marker ge
7	274	100.0	362	8	ADP12500	Adp12500 Protein e
8	274	100.0	442	7	ADJ70081	Adj70081 Human hea
9	250	91.2	677	4	ABG26726	Abg26726 Novel hum
10	241	88.0	271	3	AAB43986	Aab43986 Human can
11	215	78.5	215	4	AGG64619	Agg64619 Human can
12	215	78.5	215	7	ADP55589	Adp55589 Fragment
13	99	36.1	120	3	AGS0209	Agso209 Human sec
14	70	25.5	186	5	ABF42931	Abf42931 Human ova
15	68	24.8	96	8	ABO57084	Abos7084 Human gen
16	44	16.1	77	8	ABO60639	Abos60639 Human gen
17	44	16.1	104	3	ABO57455	Abos7455 Human gen
18	44	16.1	104	3	ABP58497	Abp58497 Lung canc
19	44	16.1	274	1	ABP80911	Abp80911 Consensu
20	44	16.1	365	8	ADP12521	Adp12521 Protein e
21	44	16.1	366	2	ARL12466	Aril2466 HLA-C exo
22	44	16.1	366	2	AXY07033	Axy07033 Breast ca
23	44	16.1	366	7	ADL62997	Adl62997 Human apo
24	44	16.1	366	7	ADP65326	Adp65326 Human HLA
25	44	16.1	366	7	ADP65316	Adp65316 Human hla

26	44	16.1	374	4	AAO13073	Aao13073 Human pol
27	44	16.1	380	4	AAU32883	Aau32883 Novel hum
28	43	15.7	120	4	AAB90793	Aab90793 Human she
29	43	15.7	130	5	ADI80341	Adi80341 Human leu
30	43	15.7	362	7	ADE31177	Ade31177 Human dia
31	40	14.6	78	8	ABO57118	Abos7118 Human gen
32	40	14.6	187	8	ADP29434	Adp29434 Human sec
33	40	14.6	314	8	ADF69311	Adf69311 Human lun
34	40	14.6	371	5	ADH48788	Adh48788 NOV31 pro
35	40	14.6	371	7	ADE40250	Ade40250 Human NOV
36	39	14.2	91	4	AAU18379	Aau18379 Peptide #
37	39	14.2	91	4	ABB37410	Abb37410 Peptide #
38	39	14.2	91	4	AAU30858	Aau30858 Peptide #
39	39	14.2	91	4	ABB32163	Abb32163 Peptide #
40	39	14.2	91	4	ABB22707	Abb22707 Protein #
41	39	14.2	91	4	AAU70538	Aau70538 Human bron
42	39	14.2	91	4	AAU58091	Aau58091 Human bron
43	39	14.2	91	4	ABG52217	Abg52217 Human liv
44	39	14.2	91	4	AAU05976	Aau05976 Peptide #
45	39	14.2	91	5	ABG40192	Abg40192 Human pep

## ALIGNMENTS

RESULT 1  
ID AAG64618 standard; protein; 274 AA.  
XX

AC AAG64618;

DT 12-SEP-2001 (first entry)

DE Human cancer cell specific HLA-F antigen SEQ ID 5.

KW HLA-F antigen; cancer cell specific; human.

OS Homo sapiens.

PN JP2001095584-A.

PD 10-APR-2001.

PF 30-SEP-1999; 99JP-00279566.

PR 30-SEP-1999; 99JP-00279566.

PA (EGAW//) EGAWA K.

PA (MEDI-) MEDINET KK.

PA (KIMU/) KIMURA K.

DR WPI: 2001-360493/38.

DR N-PSDB; AAH45556.

PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.

XX Claim 2; Page 10-11; 12pp; Japanese.

CC This invention relates to a cancer cell specific HLA-F antigen. The  
CC invention includes DNA encoding the antigen, and a method for the  
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
CC used in a method to diagnose cancer, in which the protein is used to  
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
CC sequence represents the cancer cell-specific HLA-F antigen of the  
CC invention

XX Sequence 274 AA;

Query Match 100.0%; Score 274; DB 4; Length 274;

Best Local Similarity 100.0%; Pred. No. 7.5e-250;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRGRGEPRIAYEVDDTQFLRFDSDAAPRMBPREFWQEGPQYW 60

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Db 1 GSHSLRFTSTAVSRPGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Qy 61 EWTGAYAKANAQTDVALRNLRRYNSQSEAGSHTLQMGNGCDMGPDGGLLRGYHQHAYDG 120
Db 61 GSHSLRFTSTAVSRPGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Qy 61 EWTGAYAKANAQTDVALRNLRRYNSQSEAGSHTLQMGNGCDMGPDGGLLRGYHQHAYDG 120
Qy 121 KYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Db 121 KYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Qy 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQRDGEEQOTDELVEVTRPAGDGT 240
Db 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQRDGEEQOTDELVEVTRPAGDGT 240
Qy 241 FQKWAUVVPSGEEQRYTCHVQHEGLPOPLILRW 274
Db 241 FQKWAUVVPSGEEQRYTCHVQHEGLPOPLILRW 274

RESULT 2
ADF55588
ID ADF55588 standard; protein; 274 AA.
XX AC ADF55588;
XX DT 12-FEB-2004 (first entry)
XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.
XX KW Cancer; human leukocyte antigen-F; HLA-F;
XX KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
XX KW major histocompatibility complex; MHC; cancer cell; human.
XX OS Homo sapiens.
XX PN JP2003012544-A.
XX PD 15-JAN-2003.
XX PF 27-MAR-2002; 2002JP-00088991.
XX PR 27-MAR-2001; 2001JP-00090121.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA Y.
XX DR WPI; 2003-486263/46.
XX DR N-PSDB; ADF55585.
XX PT Agent for preventing and treating cancer, comprising human leukocyte
XX antigen-F DNA, or a plasmid or viral vector comprising the DNA.
XX PS Claim 7; SEQ ID NO 5; 19pp; Japanese.
XX CC The present invention relates to an agent for preventing or treating
XX cancer. The agent comprises a portion or a complete sequence of a human
XX leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
XX presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
XX a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
XX (CTL) inducer which induces CTL which is non-specific to an organ, is
XX CC unrestricted to the major histocompatibility complex (MHC) and specific
XX to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
XX is useful for treating or preventing cancer. A cell capable of presenting
XX a cancer-cell specific antigen is useful for measuring HLA-F antigen and
XX for diagnosing cancer. The present sequence represents part of the human
XX cancer-cell specific HLA-F antigen.
XX SQ Sequence 274 AA;
Query Match 100.0%; Score 274; DB 7; Length 274;
Best Local Similarity 100.0%; Pred. No. 7.5e-250;

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Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GSHSLRFTSTAVSRPGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Db 1 GSHSLRFTSTAVSRPGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Qy 61 EWTGAYAKANAQTDVALRNLRRYNSQSEAGSHTLQMGNGCDMGPDGGLLRGYHQHAYDG 120
Db 61 EWTGAYAKANAQTDVALRNLRRYNSQSEAGSHTLQMGNGCDMGPDGGLLRGYHQHAYDG 120
Qy 121 KYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Db 121 KYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Qy 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQRDGEEQOTDELVEVTRPAGDGT 240
Db 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQRDGEEQOTDELVEVTRPAGDGT 240
Qy 241 FQKWAUVVPSGEEQRYTCHVQHEGLPOPLILRW 274
Db 241 FQKWAUVVPSGEEQRYTCHVQHEGLPOPLILRW 274

RESULT 3
AAG64617
ID AAG64617 standard; protein; 362 AA.
XX AC AAG64617;
XX DT 12-SEP-2001 (first entry)
XX DE Human cancer cell specific HLA-F antigen SEQ ID 4.
XX KW HLA-F antigen; cancer cell specific; human.
XX OS Homo sapiens.
XX PN JP2001095584-A.
XX PD 10-APR-2001.
XX PF 30-SEP-1999; 99JP-00279566.
XX PR 30-SEP-1999; 99JP-00279566.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA K.
XX DR WPI; 2001-360493/38.
XX DR N-PSDB; AAG45555.
XX PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX PS Disclosure; Page 9-10; 12pp; Japanese.
XX CC This invention relates to a cancer cell specific HLA-F antigen. The
XX invention includes DNA encoding the antigen, and a method for the
XX preparation of the cancer cell specific HLA-F antigen. The antigen may be
XX used in a method to diagnose cancer, in which the protein is used to
XX detect anti-HLA-F antibodies in bodily fluids of the patient. The present
XX CC sequence represents the cancer cell-specific HLA-F antigen of the
XX invention.
XX SQ Sequence 362 AA;
Query Match 100.0%; Score 274; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 9.4e-250;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GSHSLRFTSTAVSRPGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Db 22 GSHSLRFTSTAVSRPGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 81

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QY 61 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLLRLGYHQHAYDG 120  
 DB 82 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLLRLGYHQHAYDG 141  
 QY 121 KYISLNEDLSRWTAADTVAQITQRFYAEYAEFFRYLEGECELELLRRLYLENGKETLQ 180  
 DB 142 KYISLNEDLSRWTAADTVAQITQRFYAEYAEFFRYLEGECELELLRRLYLENGKETLQ 201  
 QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQOTELVETRPAGDGT 240  
 DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQOTELVETRPAGDGT 261  
 QY 241 FOKWAAVVPSEGEORYTCHVQHEGLPQPLILRW 274  
 DB 262 FOKWAAVVPSEGEORYTCHVQHEGLPQPLILRW 295

## RESULT 4

ABB50296  
 ID ABB50296 standard; protein; 362 AA.

XX AC ABB50296;

XX DT 08-FEB-2002 (first entry)

XX DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.

XX KW Ovarian tumour marker gene; human; overexpression; upregulation;  
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;  
 KW identification; serous cystadenoma; borderline serous tumour;  
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;  
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;  
 KW adenosifibroma; Brenner tumour; serial analysis of gene expression; SAGE;  
 KW immune response pathway; cell proliferation regulation; protein folding;  
 KW membrane localised; secreted; therapeutic target; cytosolic;  
 KW gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200175177-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010947.

XX PR 03-APR-2000; 2000US-0194336P.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;

XX DR WPI; 2001-626450/72.

XX DR N-PSDB; ABA83122.

XX PT Detecting and identifying ovarian tumor, identifying increased risk for  
 PT developing ovarian cancer, and determining effectiveness of ovarian  
 PT cancer treatment, by measuring expression level of ovarian tumor marker  
 PT gene.

XX PS Claim 23; Page 126-127; 140pp; English.

XX CC The invention relates to methods for diagnosing and prognosing ovarian  
 CC tumours in an individual via the detection and measurement of the  
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,  
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,  
 CC ABA83181 and ABA83183). The methods of the invention are useful for  
 CC detecting an ovarian tumour in a patient, for identifying an individual  
 CC at increased risk for developing ovarian cancer, in prognostic tests for  
 CC assessing the relative severity of ovarian cancer, in tests for  
 CC monitoring a patient in remission from ovarian cancer, and in tests for  
 CC monitoring disease status in a patient being treated for ovarian cancer.

CC The methods can additionally be used to identify a particular tumour as  
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from  
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,  
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous  
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,  
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner  
 CC tumour. The ovarian tumour marker genes of the invention were identified  
 CC using SAGE (serial analysis of gene expression) and were found to be  
 CC overexpressed in a broad variety of ovarian epithelial tumour cells  
 CC relative to normal ovarian epithelial cells. The marker genes are  
 CC implicated in immune response pathways, in the regulation of cell  
 CC proliferation and in protein folding, and many of these are membrane-  
 CC localised or secreted. In addition to their use as diagnostic and  
 CC prognostic markers, the ovarian tumour marker genes or their encoded  
 CC proteins may be used as therapeutic targets for the treatment and  
 CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent  
 CC proteins encoded by ovarian tumour marker genes of the invention

XX SQ Sequence 362 AA;

Query Match 100.0%; Score 274; DB 4; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-250;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGERYIAVEYVDDTQFLRPSDAAIPRMEPREPWQEGPQYW 60

DB 22 GSHSLRYFSTAVSRPGEGERYIAVEYVDDTQFLRPSDAAIPRMEPREPWQEGPQYW 81

QY 61 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLLRLGYHQHAYDG 120

DB 82 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLLRLGYHQHAYDG 141

QY 121 KYISLNEDLSRWTAADTVAQITQRFYAEYAEFFRYLEGECELELLRRLYLENGKETLQ 180

DB 142 KYISLNEDLSRWTAADTVAQITQRFYAEYAEFFRYLEGECELELLRRLYLENGKETLQ 201

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQOTELVETRPAGDGT 240

DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQOTELVETRPAGDGT 261

QY 241 FOKWAAVVPSEGEORYTCHVQHEGLPQPLILRW 274

DB 262 FOKWAAVVPSEGEORYTCHVQHEGLPQPLILRW 295

## RESULT 5

ADF55587

ID ADF55587 standard; protein; 362 AA.

XX AC ADF55587;

XX DT 12-FEB-2004 (first entry)

XX DE Human cancer-cell specific HLA-F antigen.

XX KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.

XX OS Homo sapiens.

XX PN JP2003012544-A.

XX PD 15-JAN-2003.

XX PF 27-MAR-2002; 2002JP-00088991.

XX PR 27-MAR-2001; 2001JP-00090121.

XX PA (EGAW/) EGAWA K.

XX PA (MEDI-) MEDINET KK.

XX PA (KIMU/) KIMURA Y.

DR WPI; 2003-486263/46.  
 DR N-PSDB; ADF55584.  
 XX  
 PT Agent for preventing and treating cancer, comprising human leukocyte  
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
 XX  
 PS Claim 5; SEQ ID NO 4; 19pp; Japanese.  
 XX  
 CC The present invention relates to an agent for preventing or treating  
 CC cancer. The agent comprises a portion or a complete sequence of a human  
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
 CC unrestricted to the major histocompatibility complex (MHC) and specific  
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
 CC is useful for treating or preventing cancer. A cell capable of presenting  
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
 CC for diagnosing cancer. The present sequence represents human cancer-cell  
 CC specific HLA-F antigen.  
 XX  
 SQ Sequence 362 AA;  
 Query Match 100.0%; Score 274; DB 7; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-250;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPEPPEPFWVEQGPQYW 60  
 DB 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPEPPEPFWVEQGPQYW 81  
 QY 61 EWTGKAKNAQTDVALNLLRRYNQSEAGSHTLQMGCDGPDGRLRGYHGHAYDG 120  
 DB 82 EWTGKAKNAQTDVALNLLRRYNQSEAGSHTLQMGCDGPDGRLRGYHGHAYDG 141  
 QY 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFEFTYLEGECLELLRRYLENGKETLQ 180  
 DB 142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFEFTYLEGECLELLRRYLENGKETLQ 201  
 QY 181 RADPPKAAHVAHPISDNEATLRCWALGFYPAEITLTWQRDGEQOTDTLVEVTRPAGDGT 240  
 DB 202 RADPPKAAHVAHPISDNEATLRCWALGFYPAEITLTWQRDGEQOTDTLVEVTRPAGDGT 261  
 QY 241 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 274  
 DB 262 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 295  
 RESULT 6  
 ADJ75372  
 ID ADJ75372 standard; protein; 362 AA.  
 XX  
 AC ADJ75372;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Marker gene related amino acid sequence SEQ ID NO:624.  
 XX  
 KW bronchial asthma; chronic obstructive pulmonary disease;  
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
 KW gene therapy; marker.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI394274-A2.  
 XX  
 PD 03-MAR-2004.  
 XX  
 PF 04-AUG-2003; 2003EP-00254857.  
 XX  
 PR 06-AUG-2002; 2003JP-00229312.  
 PR 20-MAR-2003; 2003JP-00077212.  
 XX

(GENO-) GENOX RES INC.  
 Ontani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;  
 WPI; 2004-193155/19.  
 XX  
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by  
 PT comparing the expression level of a marker gene in a biological sample  
 PT from a subject with the expression level of the gene in a sample from a  
 PT healthy subject.  
 XX  
 PS Example 11; SEQ ID NO 624; 241pp; English.  
 XX  
 CC The present invention describes a method of testing for bronchial asthma  
 CC or chronic obstructive pulmonary disease. The method comprises  
 CC determining the expression level of a marker gene in a biological sample  
 CC from a subject, comparing the expression level determined with the  
 CC expression level of the marker gene in a biological sample from a healthy  
 CC subject, and judging whether the subject has bronchial asthma or chronic  
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
 CC genes (S1) whose expression levels increase when respiratory epithelial  
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
 CC whose expression levels decrease when respiratory epithelial cells are  
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
 CC (2) a kit for screening for a candidate compound for a therapeutic agent  
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
 CC an animal model for bronchial asthma or chronic obstructive pulmonary  
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
 CC method for producing an animal model for bronchial asthma or chronic  
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
 CC a marker gene or an antisense nucleic acid corresponding to a portion of  
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
 CC expression of the gene through an RNAi effect or an antibody recognising  
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
 CC probe has been immobilised to assay a marker gene. (I) has respiratory  
 CC and antiasthmatic activities, and can be used in gene therapy. The method  
 CC is useful for testing for or screening for a therapeutic agent for  
 CC bronchial asthma or chronic obstructive pulmonary disease. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 362 AA;  
 Query Match 100.0%; Score 274; DB 8; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-250;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPEPPEPFWVEQGPQYW 60  
 DB 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPEPPEPFWVEQGPQYW 81  
 QY 61 EWTGKAKNAQTDVALNLLRRYNQSEAGSHTLQMGCDGPDGRLRGYHGHAYDG 120  
 DB 82 EWTGKAKNAQTDVALNLLRRYNQSEAGSHTLQMGCDGPDGRLRGYHGHAYDG 141  
 QY 121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFEFTYLEGECLELLRRYLENGKETLQ 180  
 DB 142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFEFTYLEGECLELLRRYLENGKETLQ 201  
 QY 181 RADPPKAAHVAHPISDNEATLRCWALGFYPAEITLTWQRDGEQOTDTLVEVTRPAGDGT 240  
 DB 202 RADPPKAAHVAHPISDNEATLRCWALGFYPAEITLTWQRDGEQOTDTLVEVTRPAGDGT 261  
 QY 241 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 274  
 DB 262 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 295  
 RESULT 7  
 ADP12500  
 ID ADP12500 standard; protein; 362 AA.

XX AC ADP12500;  
 XX DT 12-AUG-2004 (first entry)  
 XX DE Protein encoded by mRNA of the invention #110.  
 XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;  
 XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.  
 XX OS Homo sapiens.  
 XX PN WO2004042346-A2.  
 XX PD 21-MAY-2004.  
 XX PF 24-APR-2003; 2003WO-US012946.  
 XX PR 24-APR-2002; 2002US-00131831.  
 XX PR 20-DEC-2002; 2002US-00325899.  
 XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 XX PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;  
 XX PI Rosenberg S;  
 XX DR WPI; 2004-400724/37.  
 XX PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,  
 XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant  
 XX PT rejection, in an individual, comprises detecting the expression level of  
 XX PT the genes.  
 XX PS Claim 65; SEQ ID NO 2509; 1762pp; English.  
 XX CC The present invention relates to diagnosing or monitoring transplant  
 XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual  
 XX CC comprising detecting the expression level of one or more genes. The  
 XX CC methods, system and kits are useful in diagnosing or monitoring  
 XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic  
 XX CC islet, lung, bone marrow or stem cell transplant rejection,  
 XX CC xenotransplant rejection or mechanical organ replacement rejection, in an  
 XX CC individual. The method is also useful in assessing the immune status of  
 XX CC an individual. The methods are also useful in diagnosing and monitoring  
 XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,  
 XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or  
 XX CC viral, bacterial or fungal infection. The present sequence represents a  
 XX CC protein that is encoded by the mRNA of the invention.  
 XX SQ Sequence 362 AA;  
 Query Match 100.0%; Score 274; DB 8; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-250;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSHSLRYFTAVSRGRGEPRIAYEYVDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 60  
 DB 22 GSHSLRYFTAVSRGRGEPRIAYEYVDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 81  
 QY 61 EMTTGAKANAQTDRAVLENNLLRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQYADG 120  
 DB 82 EMTTGAKANAQTDRAVLENNLLRYNQSEAGSHTLQGNMGCDMGPDGRLRGYHQYADG 141  
 QY 121 KYIISNEDLRSWTAAVTAQITQFYAEYAEFRYTLQEGCELELLRYLNGKETLQ 180  
 DB 142 KYIISNEDLRSWTAAVTAQITQFYAEYAEFRYTLQEGCELELLRYLNGKETLQ 201  
 QY 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTQTELVEFRPAGDGT 240  
 DB 202 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTQTELVEFRPAGDGT 261  
 QY 241 FQKWAAVVPSGEGORYTCHVQHEGLPQPLILRW 274

DB 262 FQKWAAVVPSGEGORYTCHVQHEGLPQPLILRW 295  
 RESULT 8  
 ADJ70081  
 ID ADJ70081 standard; protein; 442 AA.  
 XX AC ADJ70081;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Human heat mitochondrial protein as a therapeutic target SeqID1897.  
 XX KW mitochondrial; human; screening assay; diabetes mellitus;  
 XX KW Huntington's disease; osteoarthritis; LHON;  
 XX KW Leber's hereditary optic neuropathy; LHON;  
 XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 XX KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
 XX KW osteopathic; ophthalmological; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO2003087768-A2.  
 XX PD 23-OCT-2003.  
 XX PF 04-APR-2003; 2003WO-US010870.  
 XX PR 12-APR-2002; 2002US-0372843P.  
 XX PR 17-JUN-2002; 2002US-0389987P.  
 XX PR 20-SEP-2002; 2002US-0412418P.  
 XX PA (MITO-) MITOKOR.  
 XX PA (BUCK-) BUCK INST AGE RES.  
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
 XX PI Warnock DE;  
 XX DR WPI; 2003-845369/78.  
 XX PT Identifying a mitochondrial target for drug screening assays and for  
 XX PT treating diseases associated with altered mitochondrial function,  
 XX PT comprises detecting a modified polypeptide in a sample and correlating  
 XX PT with the disease.  
 XX PS Claim 1; SEQ ID NO 1897; 180pp; English.  
 XX CC This invention relates to novel mitochondrial targets that can be used  
 XX CC for therapeutic intervention in treating a disease associated with  
 XX CC altered mitochondrial function. Specifically, it refers to a method for  
 XX CC identifying proteins of the human heart mitochondrial proteome that are  
 XX CC useful for drug screening assays, as well as therapeutic targets. The  
 XX CC present invention describes a method for identifying such proteins that  
 XX CC can be used in the treatment of various diseases associated with altered  
 XX CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 XX CC compositions have neuroprotective, nontropic, antidiabetic,  
 XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 XX CC cytostatic activities. This polypeptide sequence is a human heart  
 XX CC mitochondrial protein of the invention.  
 XX SQ Sequence 442 AA;  
 Query Match 100.0%; Score 274; DB 7; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-249;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSHSLRYFTAVSRGRGEPRIAYEYVDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 60  
 DB 22 GSHSLRYFTAVSRGRGEPRIAYEYVDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 81

QY 61 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMGDPDGLLRGYHQHAYDG 120  
 DB 82 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMGDPDGLLRGYHQHAYDG 141  
 QY 121 KQYISLNEDLSRWTAADTVAQITQRFYEAEBYAEFRTYLGECLELLRYLNGKETLQ 180  
 DB 142 KQYISLNEDLSRWTAADTVAQITQRFYEAEBYAEFRTYLGECLELLRYLNGKETLQ 201  
 QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 240  
 DB 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 261  
 QY 241 FQKWAAVVPSGEORVTCVQHEGLPOPLILRW 274  
 DB 262 FQKWAAVVPSGEORVTCVQHEGLPOPLILRW 295

RESULT 9  
 ID ABG26726 standard; protein; 677 AA.  
 AC ABG26726;  
 XX  
 DT 18-FEB-2002 (first entry)  
 DE  
 XX Novel human diagnostic protein #26717.  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175087-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Drmanac RT, Liu C, Tang YT;  
 XX  
 XX WPI; 2001-639362/73.  
 DR N-PSDB; AAS90913.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 XX Claim 20; SEQ ID NO 57085; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have application of mutations  
 CC in diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 677 AA;

Query Match 91.2%; Score 250; DB 4; Length 677;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-227;  
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGRCGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 60  
 DB 331 GSHSLRYFSTAVSRGRCGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 390  
 QY 61 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMGDPDGLLRGYHQHAYDG 120  
 DB 391 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMGDPDGLLRGYHQHAYDG 450  
 QY 121 KQYISLNEDLSRWTAADTVAQITQRFYEAEBYAEFRTYLGECLELLRYLNGKETLQ 180  
 DB 451 KQYISLNEDLSRWTAADTVAQITQRFYEAEBYAEFRTYLGECLELLRYLNGKETLQ 510  
 QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 240  
 DB 511 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 570  
 QY 241 FQKWAAVVVP 250  
 DB 571 FQKWAAVVVP 580

RESULT 10  
 AAB43986  
 ID AAB43986 standard; protein; 271 AA.  
 XX  
 AC AAB43986;  
 XX  
 DT 08-FEB-2001 (first entry)  
 DE  
 XX Human cancer associated protein sequence SEQ ID NO:1431.  
 XX Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antithyroid; antiviral;  
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipariatic; antidiabetic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055350-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005882.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM;  
 PI  
 XX WPI; 2000-587533/55.  
 DR N-PSDB; AAC78195.  
 XX  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.  
 XX

PS Claim 11; Page 2115-2116; 2352pp; English.  
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB43398 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; tumorigenic; immunomodulatory;  
 CC antidiabetic; antihypertensive; antirheumatic; antithrombotic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
 CC neoplastic; vasotropic; antipsoriatic and angiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilization of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 CC  
 SQ Sequence 271 AA;

Query Match 88.0%; Score 241; DB 3; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-219;  
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSHSLRYSTAVSRGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 60  
 DB 28 GSHSLRYSTAVSRGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 87  
 QY 61 EMTTGYAKANAOTDVALNLLRRYNOSEAGSHTLQGMNGCDMPDGLLRGYHAYDG 120  
 DB 88 EMTTGYAKANAOTDVALNLLRRYNOSEAGSHTLQGMNGCDMPDGLLRGYHAYDG 147  
 QY 121 KYIISLNEDLRSWTAADTVAQITQRYEAEYAEFRYLEGECELELLRRYLENGKETLQ 180  
 DB 148 KYIISLNEDLRSWTAADTVAQITQRYEAEYAEFRYLEGECELELLRRYLENGKETLQ 207  
 QY 181 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEQOTQTELVEPTRAGDT 240  
 DB 208 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEQOTQTELVEPTRAGDT 267  
 QY 241 F 241  
 DB 268 F 268

RESULT 11  
 ID AAG64619 standard; protein; 215 AA.  
 AC AAG64619;  
 XX  
 XX 12-SEP-2001 (first entry)  
 DT  
 DE Human cancer cell specific HLA-F antigen SEQ ID 6.  
 XX  
 XX HLA-F antigen; cancer cell specific; human.  
 KW  
 XX Homo sapiens.  
 OS  
 XX JP2001095584-A.  
 PN  
 XX 10-APR-2001.  
 PD  
 XX 30-SEP-1999; 99JP-00279566.  
 PF  
 XX 30-SEP-1999; 99JP-00279566.  
 PR  
 XX  
 XX

PA (EGAW/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 XX (KIMU/) KIMURA K.  
 DR WPI; 2001-360493/38.  
 DR N-PSDB; AAB45557.  
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
 XX Claim 1; Page 11-12; 12pp; Japanese.  
 XX This invention relates to a cancer cell specific HLA-F antigen. The  
 CC invention includes DNA encoding the antigen, and a method for the  
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
 CC used in a method to diagnose cancer, in which the protein is used to  
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
 CC sequence represents the cancer cell-specific HLA-F antigen of the  
 CC invention  
 XX  
 SQ Sequence 215 AA;  
 Query Match 78.5%; Score 215; DB 4; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-194;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWETTYAKANAOTDVALNLL 82  
 DB 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWETTYAKANAOTDVALNLL 60  
 QY 83 PRYNOSEAGSHTLQGMNGCDMPDGLLRGYHAYDGKDYIISLNEDLRSWTAADTVAQI 142  
 DB 61 PRYNOSEAGSHTLQGMNGCDMPDGLLRGYHAYDGKDYIISLNEDLRSWTAADTVAQI 120  
 QY 143 TORFYAEAEYAEFRYLEGECELELLRRYLENGKETLQRADPPKHAHVHPIISDHEATL 202  
 DB 121 TORFYAEAEYAEFRYLEGECELELLRRYLENGKETLQRADPPKHAHVHPIISDHEATL 180  
 QY 203 CWNLGFYPAEITLTWQDGEQOTQTELVEPTRAG 237  
 DB 181 CWNLGFYPAEITLTWQDGEQOTQTELVEPTRAG 215  
 RESULT 12  
 ADF55589  
 ID ADF55589 standard; protein; 215 AA.  
 AC ADF55589;  
 XX  
 XX 12-FEB-2004 (first entry)  
 DT  
 DE Fragment #2 of human cancer-cell specific HLA-F antigen.  
 XX  
 XX Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP2003012544-A.  
 PN  
 XX 15-JAN-2003.  
 PD  
 XX 27-MAR-2002; 2002JP-00088891.  
 PF  
 XX 27-MAR-2001; 2001JP-00090121.  
 PR  
 XX (EGAW/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU/) KIMURA Y.  
 XX  
 DR WPI; 2003-486263/46.  
 DR N-PSDB; ADF55586.  
 XX

PT Agent for preventing and treating cancer, comprising human leukocyte  
XX antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
PS Claim 7; SEQ ID NO 6; 19pp; Japanese.  
XX  
CC The present invention relates to an agent for preventing or treating  
CC cancer. The agent comprises a portion or a complete sequence of a human  
CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
CC unrestricted to the major histocompatibility complex (MHC) and specific  
CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
CC is useful for treating or preventing cancer. A cell capable of presenting  
CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
CC for diagnosing cancer. The present sequence represents part of the human  
CC cancer-cell specific HLA-F antigen.  
XX  
SQ Sequence 215 AA;

Query Match 78.5%; Score 215; DB 7; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.7e-194;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 23 IAVEVDVDTQFLRPSDAAIPRMEPEPVEQSGPOYWEWTCYAKANAQTDVLRNLL 82  
DB 1 IAVEVDVDTQFLRPSDAAIPRMEPEPVEQSGPOYWEWTCYAKANAQTDVLRNLL 60  
QY 83 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHGHAYDGRDYISLNEDELSMTAADTVAQI 142  
DB 61 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHGHAYDGRDYISLNEDELSMTAADTVAQI 120  
QY 143 TORFEAEVAAEFRTYLEGECELELRRYLENGKETLORADPPKARVAHHPISDHEATLR 202  
DB 121 TORFEAEVAAEFRTYLEGECELELRRYLENGKETLORADPPKARVAHHPISDHEATLR 180  
QY 203 CWALGFYPAEITLTWQRDGEQTDTELVTETPAG 237  
DB 181 CWALGFYPAEITLTWQRDGEQTDTELVTETPAG 215

RESULT 13  
AAG00209  
ID AAG00209 standard; protein; 120 AA.  
XX  
AC AAG00209;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein, SEQ ID NO: 4290.  
XX  
KW Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX  
OS Homo sapiens.  
XX  
PN EPI033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-00200610.  
XX  
PR 26-FEB-1999; 99US-0122487P.  
XX  
PA (GIST ) GENSET.  
XX  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
DR WPI; 2000-500381/45.  
DR N-PSDB; AAC00215.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.  
XX  
CC The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors  
XX  
SQ Sequence 120 AA;

Query Match 36.1%; Score 99; DB 3; Length 120;  
Best Local Similarity 100.0%; Pred. No. 4.3e-85;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GHSRLRYFSTAVSRGCRGEPRIAYVEYVDDTQFLRPSDAAIPRMEPEPVEQSGPOYW 60  
DB 22 GHSRLRYFSTAVSRGCRGEPRIAYVEYVDDTQFLRPSDAAIPRMEPEPVEQSGPOYW 81  
QY 61 EMTTGVAKANAQTDVLRNLLRRYNQSEAGSHTLQGMN 99  
DB 82 EMTTGVAKANAQTDVLRNLLRRYNQSEAGSHTLQGMN 120

RESULT 14  
ABP42931  
ID ABP42931 standard; protein; 186 AA.  
XX  
AC ABP42931;  
XX  
DT 22-AUG-2002 (first entry)  
XX  
DE Human ovarian antigen HPRDRT37, SEQ ID NO:4063.  
XX  
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive.  
XX  
OS Homo sapiens.  
XX  
PN WO200200677-A1.  
XX  
PD 03-JAN-2002.  
XX  
PF 07-JUN-2001; 2001WO-US018569.  
XX  
PR 07-JUN-2000; 2000US-0209467P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Birse CE, Rosen CA;  
XX  
DR WPI; 2002-147878/19.  
DR N-PSDB; ABQ56008.  
XX  
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian

cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 11; SEQ ID NO 4063; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovarian and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 186 AA;

Query Match 25.5%; Score 70; DB 5; Length 186;  
Best Local Similarity 100.0%; Pred. No. 1.3e-57;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

66 YAKANAQTDVVALNRLRYNQSEAGSHTLQGMGCDMGDPGRLLRGYHQHAYDGDYIS 125  
1 YAKANAQTDVVALNRLRYNQSEAGSHTLQGMGCDMGDPGRLLRGYHQHAYDGDYIS 60

126 LNEDLSWTA 135

61 LNEDLSWTA 70

RESULT 15

ID ABO57084

XX ABO57084 standard; protein; 96 AA.

AC ABO57084;

XX 29-JUL-2004 (first entry)

DE Human genome derived single exon protein #3318.

XX Human; gene expression; single exon probe; microarray;

KN alternative splicing event; genomic alteration.

XX Homo sapiens.

OS US2003194704-A1.

PN 16-OCT-2003.

PD 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX

PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

XX Claim 45; SEQ ID NO 30718; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 96 AA;

Query Match 24.8%; Score 68; DB 8; Length 96;

Best Local Similarity 100.0%; Pred. No. 6.1e-56;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 DPPKHAHVAHPISDHEATLRCWALGFYPARITLTWQDGEQQTDELVETRPAGDGTQ 242

Db 2 DPPKHAHVAHPISDHEATLRCWALGFYPARITLTWQDGEQQTDELVETRPAGDGTQ 61

QY 243 KWAAYVVP 250

Db 62 KWAAYVVP 69

Search completed: December 15, 2004, 18:20:02

Job time : 125.151 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 18:24:34 ; Search time 111.505 Seconds  
(without alignments)  
877.689 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYFSTAVSRPGRGP.....QRYTCHVQHGELPQLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1585576 seqs, 357178320 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	274	100.0	274	11	US-09-819-371-5
2	274	100.0	362	14	US-10-257-021-82
3	274	100.0	442	16	US-10-408-765A-1887
4	241	88.0	271	9	US-09-925-301-1431
5	175	63.9	362	11	US-09-819-371-4
6	119	43.4	215	11	US-09-819-371-6
7	70	25.5	186	15	US-10-264-049-4063
8	68	24.8	96	14	US-10-029-386-30718
9	44	16.1	77	14	US-10-029-386-34273
10	44	16.1	91	14	US-10-029-386-31089
11	44	16.1	104	9	US-09-925-302-835
12	44	16.1	104	10	US-09-925-302-835
13	43	15.7	476	17	US-10-430-984-16

14	43	15.7	500	17	US-10-430-984-15	Sequence 15, Appl
15	40	14.6	78	14	US-10-029-386-30752	Sequence 30752, A
16	40	14.6	371	15	US-10-085-198-72	Sequence 72, Appl
17	40	14.6	371	15	US-10-210-172-156	Sequence 156, App
18	39	14.2	91	9	US-09-864-761-38005	Sequence 38005, A
19	39	14.2	92	15	US-10-380-880-5	Sequence 5, Appl
20	39	14.2	169	16	US-10-741-601-383	Sequence 383, App
21	39	14.2	198	16	US-10-741-601-387	Sequence 387, App
22	39	14.2	234	15	US-10-380-880-8	Sequence 8, Appl
23	39	14.2	251	16	US-10-741-601-384	Sequence 384, App
24	39	14.2	284	14	US-10-104-047-3648	Sequence 3648, App
25	39	14.2	326	15	US-10-380-880-7	Sequence 7, Appl
26	39	14.2	338	16	US-10-741-601-380	Sequence 380, App
27	39	14.2	338	16	US-10-741-601-388	Sequence 388, App
28	39	14.2	343	16	US-10-741-601-379	Sequence 379, App
29	39	14.2	379	14	US-10-093-463-78	Sequence 78, Appl
30	39	14.2	379	15	US-10-210-172-160	Sequence 160, App
31	38	13.9	145	9	US-09-810-560-8	Sequence 8, Appl
32	36	13.1	45	14	US-10-029-386-28883	Sequence 28883, A
33	32	11.7	91	9	US-09-864-761-35461	Sequence 35461, A
34	32	11.7	110	9	US-09-796-692-799	Sequence 799, App
35	32	11.7	110	9	US-09-796-692-2139	Sequence 2139, App
36	32	11.7	110	14	US-10-040-862-799	Sequence 799, App
37	32	11.7	110	14	US-10-040-862-2139	Sequence 2139, App
38	32	11.7	110	15	US-10-057-4758-799	Sequence 799, App
39	32	11.7	110	15	US-10-057-4758-2139	Sequence 2139, App
40	32	11.7	110	15	US-10-154-884B-799	Sequence 799, App
41	32	11.7	110	15	US-10-154-884B-2139	Sequence 2139, App
42	32	11.7	110	16	US-10-764-324-799	Sequence 799, App
43	32	11.7	110	16	US-10-764-324-2139	Sequence 2139, App
44	32	11.7	196	15	US-10-262-839-48	Sequence 48, Appl
45	32	11.7	198	15	US-10-264-049-3505	Sequence 3505, App

## ALIGNMENTS

### RESULT 1

US-09-819-371-5  
; Sequence 5, Application US/09819371  
; Publication No. US2004005344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 5  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-5

Query Match 100.0%; Score 274; DB 11; Length 274;  
Best Local Similarity 100.0%; Pred. No. 2.6e-260;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GSHSLRYFSTAVSRPGRGPRIAYEVYDPTQFLRFDSDAAIPRMPRPFWVEQGPQYW	60
Db	1	GSHSLRYFSTAVSRPGRGPRIAYEVYDPTQFLRFDSDAAIPRMPRPFWVEQGPQYW	60
QY	61	EWTTGYAKANQDTRVALRNLRLRYNOSAGSHTLQMGNCMDGPDGRLLRGVHQHAYDG	120
Db	61	EWTTGYAKANQDTRVALRNLRLRYNOSAGSHTLQMGNCMDGPDGRLLRGVHQHAYDG	120
QY	121	KDYISLNEELRSWTAADTAQITQRFYEABEYAEFRTYLEGECLELLRRLYENKGTTLQ	180
Db	121	KDYISLNEELRSWTAADTAQITQRFYEABEYAEFRTYLEGECLELLRRLYENKGTTLQ	180
QY	181	RADPFKHAHVHPISDEATLRCWALGFYPAETLLTQWRDGBEQTQDTLVEFRPADGT	240

Db 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 240  
Qy 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274  
Db 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274

## RESULT 2

US-10-257-021-82  
; Sequence 82, Application US/10257021  
; Publication No. US20030211498A1  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Patrice J.  
; APPLICANT: Sherman-Baust, Cheryl A.  
; APPLICANT: Pizer, Ellen S.  
; APPLICANT: Hough, Colleen D.  
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
; FILE REFERENCE: 14014.0369U2  
; CURRENT APPLICATION NUMBER: US/10/257,021  
; PRIOR FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/10947  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/194,336  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-257-021-82

Query Match 100.0%; Score 274; DB 14; Length 362;  
Best Local Similarity 100.0%; Pred. No. 3.3e-260;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60  
Db 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 81  
Qy 61 EWTTCYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 120  
Db 82 EWTTCYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 141  
Qy 121 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 180  
Db 142 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 201  
Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 240  
Db 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 261  
Qy 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274  
Db 262 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 295

## RESULT 3

US-10-408-765A-1887  
; Sequence 1887, Application US/10408765A  
; Publication No. US2004010187A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Wainock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1887  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1887

Query Match 100.0%; Score 274; DB 16; Length 442;  
Best Local Similarity 100.0%; Pred. No. 3.9e-260;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60  
Db 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 81  
Qy 61 EWTTCYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 120  
Db 82 EWTTCYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 141  
Qy 121 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 180  
Db 142 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 201  
Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 240  
Db 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGT 261  
Qy 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274  
Db 262 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 295

## RESULT 4

US-09-925-301-1431  
; Sequence 1431, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1431  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1431

Query Match 88.0%; Score 241; DB 9; Length 271;  
Best Local Similarity 100.0%; Pred. No. 6.3e-228;  
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 60  
Db 28 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQEGPQYW 87  
Qy 61 EWTTCYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 120  
Db 88 EWTTCYAKANAQTDRAVLRNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 147  
Qy 121 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 180  
Db 148 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 207

QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVEITRPAGDGT 240  
DB 208 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVEITRPAGDGT 267  
QY 241 F 241  
DB 268 F 268

## RESULT 5

US-09-819-371-4  
; Sequence 4, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; PRIOR FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-4

Query Match 53.9%; Score 175; DB 11; Length 362;

Best Local Similarity 100.0%; Pred. No. 5.1e-163;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMPEPRPFWVEQGPQYW 60  
DB 22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMPEPRPFWVEQGPQYW 81  
QY 61 EWTTGYAKANAQTRVALNRLNRYNQSEAGSHLTQMGNCDCMPGQRLLRGHQYAYDG 120  
DB 82 EWTTGYAKANAQTRVALNRLNRYNQSEAGSHLTQMGNCDCMPGQRLLRGHQYAYDG 141  
QY 121 KDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFTYLGECLLELLRYLENG 175  
DB 142 KDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFTYLGECLLELLRYLENG 196

## RESULT 6

US-09-819-371-6  
; Sequence 6, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-6

Query Match 43.4%; Score 119; DB 11; Length 215;

Best Local Similarity 100.0%; Pred. No. 3e-108;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 DKDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFTYLGECLLELLRYLENGKET 178  
DB 97 DKDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFTYLGECLLELLRYLENGKET 156  
QY 179 LQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVEITRPAG 237

DB 157 LQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLVEITRPAG 215

## RESULT 7

US-10-264-049-4063  
; Sequence 4063, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Bitsee et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133P1  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 4063  
; LENGTH: 186  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: MISC FEATURE  
; LOCATION: (76)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (77)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (86)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (107)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (123)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (136)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (148)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (163)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (174)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (175)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (176)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:

; NAME/KEY: MISC FEATURE  
; LOCATION: (180)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-049-4063

Query Match 25.5%; Score 70; DB 15; Length 186;  
Best Local Similarity 100.0%; Pred. No. 3.4e-60;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 YAKANACTDVALRNLLRRNQSEAGSHLQNGMGDMGDPGRLLRGVHQHAYDGGKVIS 125

Db 1 YAKANACTDVALRNLLRRNQSEAGSHLQNGMGDMGDPGRLLRGVHQHAYDGGKVIS 60

Qy 126 LNEEDLSWTA 135

Db 61 LNEEDLSWTA 70

## RESULT 8

US-10-029-386-30718  
; Sequence 30718, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 30718  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR6.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12  
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52  
US-10-029-386-30718

Query Match 24.8%; Score 68; DB 14; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.7e-58;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 DPPKAVAHHPISDHEATLRCAWALGFPYPAEITLTWQDGEQTDTELVTETRPAGDGTFO 242

Db 2 DPPKAVAHHPISDHEATLRCAWALGFPYPAEITLTWQDGEQTDTELVTETRPAGDGTFO 61

Qy 243 KWAAVVVP 250

Db 62 KWAAVVVP 69

## RESULT 9

US-10-029-386-34273  
; Sequence 34273, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 34273

; LENGTH: 77  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR6.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4  
; OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42  
US-10-029-386-34273

Query Match 16.1%; Score 44; DB 14; Length 77;  
Best Local Similarity 100.0%; Pred. No. 5.1e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 267

Db 25 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 68

## RESULT 10

US-10-029-386-31089  
; Sequence 31089, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 31089  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC004204.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1  
; OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUE 1.00e-52  
US-10-029-386-31089

Query Match 16.1%; Score 44; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 5.9e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 267

Db 41 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 84

## RESULT 11

US-09-925-302-835  
; Sequence 835, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 835

QY 228 TELVTRPAGDGTGFKWAAVVPSSGEQRVTCHVOHEGLP 267  
| | | | |  
Db 29 TELVTRPAGDGTGFKWAAVVPSSGEQRVTCHVOHEGLP 68  
| | | | |

Fri Dec 17 09:27:20 2004

us-09-819-371-5.Oligo.rapb

Page 6

Search completed: December 15, 2004, 18:41:48  
Job time : 112.505 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:30 ; Search time 111.677 Seconds  
(without alignments)  
1107.709 Million cell updates/sec

Title: US-09-819-371-6  
Perfect score: 215  
Sequence: 1 TAVEYVDQTQLRFDSDAAI.....QRDGEQOTDELVEVETRPAG 215

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	55.3	324	2 Q861E9	Q861E9 homo sapien
2	119	55.3	324	2 Q861F0	Q861F0 homo sapien
3	119	55.3	346	2 Q8MGI1	Q8MGI1 homo sapien
4	119	55.3	346	2 Q8MGI2	Q8MGI2 pan troglod
5	119	55.3	346	2 Q8WLP5	Q8WLP5 homo sapien
6	119	55.3	346	2 Q8DU20	Q8DU20 homo sapien
7	119	55.3	346	2 Q8DU28	Q8DU28 homo sapien
8	119	55.3	346	2 AAR62991	AAR62991 homo sapi
9	119	55.3	362	1 HIAF HUMAN	HIAF HUMAN
10	119	55.3	362	2 Q7YR27	Q7YR27 pan troglod
11	119	55.3	362	2 BAC54915	BAC54915 homo sapi
12	119	55.3	460	2 Q85HCO	Q85HCO homo sapien
13	95	44.2	254	2 Q860R0	Q860R0 homo sapien
14	71	33.0	349	2 Q8ZUW0	Q8ZUW0 homo sapien
15	71	33.0	349	2 BAC86108	BAC86108 homo sapi
16	70	32.6	346	1 IC28 PANTR	IC28 PANTR
17	59	27.4	59	2 Q78094	Q78094 homo sapien
18	54	25.1	91	2 Q7TPX7	Q7TPX7 gorilla gor
19	53	24.7	355	2 Q767W6	Q767W6 actus trivi
20	53	24.7	355	2 BAD18842	BAD18842 actus tri
21	47	21.9	314	2 Q860F6	Q860F6 macaca neme
22	47	21.9	348	1 HIAF MACMU	HIAF MACMU
23	45	20.9	330	2 Q30713	Q30713 macaca mula
24	45	20.9	359	2 Q30711	Q30711 macaca mula
25	43	20.0	316	2 Q29958	Q29958 homo sapien
26	43	20.0	351	2 Q70PL7	Q70PL7 macaca mula
27	43	20.0	351	2 Q70PM0	Q70PM0 macaca mula
28	43	20.0	351	2 CAD89636	CAD89636 macaca mu
29	43	20.0	351	2 CAD89639	CAD89639 macaca mu
30	43	20.0	353	2 Q9MXS6	Q9MXS6 macaca mula
31	43	20.0	353	2 Q9MXS7	Q9MXS7 macaca mula

32	43	20.0	354	2 Q70S10	Q70S10 macaca mula
33	43	20.0	354	2 Q70UE5	Q70UE5 macaca mula
34	43	20.0	354	2 Q70UE6	Q70UE6 macaca mula
35	43	20.0	354	2 Q70UE7	Q70UE7 macaca mula
36	43	20.0	354	2 CAD85765	CAD85765 macaca mu
37	43	20.0	354	2 CAD85765	CAD85765 macaca mu
38	43	20.0	354	2 CAD85767	CAD85767 macaca mu
39	43	20.0	354	2 CAD83073	CAD83073 macaca mu
40	43	20.0	365	2 Q617A3	Q617A3 macaca fasc
41	43	20.0	365	2 Q9MXS5	Q9MXS5 macaca mula
42	41	19.1	330	2 Q860E9	Q860E9 macaca neme
43	41	19.1	333	2 Q860E7	Q860E7 macaca neme
44	41	19.1	337	2 Q70PK6	Q70PK6 macaca mula
45	41	19.1	337	2 CAD89650	CAD89650 macaca mu

## ALIGNMENTS

RESULT 1  
Q861E9 PRELIMINARY; PRT; 324 AA.  
AC Q861E9  
DT 01-JUN-2003 (Tremblrel. 24, Created)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE MHC class I antigen (Fragment).  
GN Name=HLA-F;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu Y., Xu L., Zeng Y., He X.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY2211102; AAC34407.1;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF07654; C1-set; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR ProDom; PD000050; MHC\_I; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
DR PROSITE; PSS0290; IG\_MHC; 1.  
FT NON\_TER 1  
FT NON\_TER 324  
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 324;  
Best Local Similarity 100.0%; Pred. No. 5.9e-117; Indels 0; Gaps 0;  
Matches 119; Conservative 0; Mismatches 0;  
QY 97 DGKDIYISLNRDLSWTAADTVAQITQFYAEAYAEFEFTYLEGECLELLRYLNGKET 156  
Db 136 DGKDIYISLNRDLSWTAADTVAQITQFYAEAYAEFEFTYLEGECLELLRYLNGKET 195  
QY 157 LQRADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEVETRPAG 215  
Db 196 LQRADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEVETRPAG 254

RESULT 2  
Q861F0 PRELIMINARY; PRT; 324 AA.  
AC Q861F0  
DT 01-JUN-2003 (Tremblrel. 24, Created)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Nonclassical MHC class I antigen (Fragment).  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA He X., Xu L., Liu Y., Zeng Y.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY216682; AAC37689.1; -.  
DR HSSP; Q29961; 1HSA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; Cl-set; 1.  
DR PRINTS; PR01638; MHC I; 1.  
DR ProDom; PD000050; MHC I; 1.  
DR SMART; SM00407; IGC1; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON-TER 324 324  
FT NON-TER 1  
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 324;  
Best Local Similarity 100.0%; Pred. No. 5.9e-117;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 DGKDYISLNEDLRSWTAADVAQITQRFYEAEYAEAEFRYLEGECLELLRRYLENGKET 156  
DB 136 DGKDYISLNEDLRSWTAADVAQITQRFYEAEYAEAEFRYLEGECLELLRRYLENGKET 195  
OY 157 LQRAADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215  
DB 196 LQRAADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 254

RESULT 3  
ID Q8MQO1 PRELIMINARY; PRT; 346 AA.  
AC Q8MQO1  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE MHC class Ib antigen.  
GN Name=HLA-F;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF523284; AA074979.1; -.  
DR EMBL; AF523291; AA074986.1; -.  
DR EMBL; AF523292; AA074987.1; -.  
DR EMBL; AF645748; AA073231.1; -.  
DR EMBL; AF645754; AA073237.1; -.  
DR HSSP; Q29961; 1HSA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC I.  
DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00129; MHC I; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR ProDom; PD000050; MHC I; 1.  
DR SMART; SM00407; IGC1; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Transmembrane.  
SQ SEQUENCE 346 AA; 39061 MW; D4782968A675B7D CRC64;

Query Match 55.3%; Score 119; DB 2; Length 346;  
Best Local Similarity 100.0%; Pred. No. 6.3e-117;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 DGKDYISLNEDLRSWTAADVAQITQRFYEAEYAEAEFRYLEGECLELLRRYLENGKET 156  
DB 140 DGKDYISLNEDLRSWTAADVAQITQRFYEAEYAEAEFRYLEGECLELLRRYLENGKET 199  
OY 157 LQRAADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215  
DB 200 LQRAADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 258

RESULT 4  
ID Q95IT2 PRELIMINARY; PRT; 346 AA.  
AC Q95IT2  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE MHC class I antigen.  
GN Name=Patr-F;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21291697; PubMed=11398964;  
RA Adams E.J., Farham P.;  
RT "Genomic analysis of common chimpanzee major histocompatibility  
complex class I genes";  
RL Immunogenetics 53:200-208(2001).  
DR EMBL; AF338355; AAK77479.1; -.  
DR HSSP; Q29961; 1HSA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0008955; P:immune response; IEA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR001039; MHC I.  
DR Pfam; PF07654; Cl-set; 1.  
DR PRINTS; PR01638; MHC I; 1.  
DR ProDom; PD000050; MHC I; 1.  
DR SMART; SM00407; IGC1; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Transmembrane.  
SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 346;  
Best Local Similarity 100.0%; Pred. No. 6.3e-117;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 DGKDYISLNEDLRSWTAADVAQITQRFYEAEYAEAEFRYLEGECLELLRRYLENGKET 156  
DB 140 DGKDYISLNEDLRSWTAADVAQITQRFYEAEYAEAEFRYLEGECLELLRRYLENGKET 199  
OY 157 LQRAADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215

Db 200 LQADPPKAAVHAHPISDHETALRCWALGFYPAEITLTWQDGEQOTDELVETRPAG 258

RESULT 5

QID Q8WLP5 PRELIMINARY; PRT; 346 AA.

AC 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE MHC class Ib antigen (HLA-F protein).

GN Name=HLA-F;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX PubMed=14705989;

RA He X., Xu L., Liu Y., Zeng Y.;

RT Identification of a novel HLA-F allele - HLA-F\*010102.;

RN [3]

RP Tissue Antigens 63:181-183 (2004).

RN [4]

RP SEQUENCE FROM N.A.

RA He X., Xu L., Liu Y., Zeng Y.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RN [5]

RP TISSUE=Lymph;

RC MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold Z.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udén T.B., Toshitoki S., Carninci P., Prange C.,

RA Baha S.S., McEwan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Hellon E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RA Strausberg R.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF523285; AAM74980.1; -

DR EMBL; AF523287; AAM74982.1; -

DR EMBL; AF523288; AAM74983.1; -

DR EMBL; AF523289; AAM74984.1; -

DR EMBL; AF523290; AAM74985.1; -

DR EMBL; AF523291; AAM74986.1; -

DR EMBL; AF523292; AAM74987.1; -

DR EMBL; AF523293; AAM74988.1; -

DR EMBL; AF523294; AAM74989.1; -

DR EMBL; AF523295; AAM74990.1; -

DR EMBL; AF523296; AAM74991.1; -

DR EMBL; AF523297; AAM74992.1; -

DR EMBL; AY253269; AA086773.1; -

DR EMBL; AY253270; AA086774.1; -

DR EMBL; EC062951; AAH62951.1; -

DR EMBL; AY645742; AAT73225.1; -

DR EMBL; AY645743; AAT73226.1; -

DR EMBL; AY645744; AAT73227.1; -

DR EMBL; AY645745; AAT73228.1; -

DR EMBL; AY645746; AAT73229.1; -

DR EMBL; AY645747; AAT73230.1; -

DR EMBL; AY645749; AAT73232.1; -

DR EMBL; AY645750; AAT73233.1; -

DR EMBL; AY645751; AAT73234.1; -

DR EMBL; AY645752; AAT73235.1; -

DR EMBL; AY645753; AAT73236.1; -

DR EMBL; AY645756; AAT73239.1; -

DR EMBL; AY645757; AAT73240.1; -

DR EMBL; AY645758; AAT73241.1; -

DR EMBL; AY645759; AAT73242.1; -

DR EMBL; AF523286; AAM74981.1; -

DR HSSP; Q23961; ILSA.

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0006955; P: immune response; IEA.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_C1.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR01039; MHC\_I.

DR Pfam; PF07654; C1-set; 1.

DR Pfam; PF00129; MHC\_I; 1.

DR PRINTS; PR01638; MHCCLASSI.

DR ProDom; PD000050; MHC\_I; 1.

DR SMART; SM00407; IGC1; 1.

DR PROSITE; PS00835; IG\_LIKE; 1.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Transmembrane.

SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 346;

Best Local Similarity 100.0%; Pred. No. 6.3e-117;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISNLDLRSWTAADTVAQITQRFYAEAEYAEFFRTYLEGCELELLRRYLENGKET 156

Db 140 DGKDYISNLDLRSWTAADTVAQITQRFYAEAEYAEFFRTYLEGCELELLRRYLENGKET 199

QY 157 LQADPPKAAVHAHPISDHETALRCWALGFYPAEITLTWQDGEQOTDELVETRPAG 215

Db 200 LQADPPKAAVHAHPISDHETALRCWALGFYPAEITLTWQDGEQOTDELVETRPAG 258

RESULT 6

QID Q6DU20 PRELIMINARY; PRT; 346 AA.

AC Q6DU20;

DT 01-OCT-2004 (TREMBlrel. 28, Created)

DT 01-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE MHC class Ib antigen.

GN Name=HLA-F;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY645755; AAT73238.1; -

SQ SEQUENCE 346 AA; 39082 MW; 6F739AA41917E7B2 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 346;

Best Local Similarity 100.0%; Pred. No. 6.3e-117;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISNLDLRSWTAADTVAQITQRFYAEAEYAEFFRTYLEGCELELLRRYLENGKET 156

Db 140 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 199  
 QY 157 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 215  
 Db 200 LQADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 258

## RESULT 7

Q6DU28 PRELIMINARY; PRT; 346 AA.  
 AC Q6DU28;  
 DT 01-OCT-2004 (TRENBLrel. 28, Created)  
 DT 01-OCT-2004 (TRENBLrel. 28, Last sequence update)  
 DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)  
 DE MHC class II antigen.  
 OS Name=HLA-F;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY645747; AAT73230.1; -  
 SQ SEQUENCE 346 AA; 39079 MW; 8C370BFB40B15818 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-117; Indels 0; Gaps 0;  
 Matches 119; Conservative 0; Mismatches 0;  
 QY 97 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 156  
 Db 140 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 199  
 QY 157 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 215  
 Db 200 LQADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 258

## RESULT 8

AAH62991 PRELIMINARY; PRT; 346 AA.  
 ID AAH62991;  
 DT 02-MAR-2004 (TRENBLrel. 27, Created)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)  
 DE HLA-F protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; Pubmed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC062991; AAH62991.1; -  
 SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-117; Indels 0; Gaps 0;  
 Matches 119; Conservative 0; Mismatches 0;  
 QY 97 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 156  
 Db 140 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 199  
 QY 157 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 215  
 Db 200 LQADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 258

## RESULT 9

HLAF HUMAN STANDARD; PRT; 362 AA.  
 ID HLAF HUMAN;  
 AC P3051l; Q9TP68;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F  
 DE antigen) (Leukocyte antigen F) (CDA12).  
 OS Name=HLA-F; Synonyms=HLAF, HLA-5.4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90111605; Pubmed=1688605;  
 RA Geraghty D.E., Wei X., Orr H.T., Koller B.H.;  
 RT "Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of  
 RT a class I coding sequence linked to a novel transcribed repetitive  
 RT element."  
 RL J. Exp. Med. 171:1-18 (1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91197889; Pubmed=1707659;  
 RA Lury D., Epstein H., Holmes N.;  
 RT "The human class I MHC gene HLA-F is expressed in lymphocytes."  
 RL Int. Immunol. 2:531-537 (1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20189617; Pubmed=10727083;  
 RA Hampe A., Coriton O., Andrieux N., Carn G., Lepourcellet M.,  
 RA Mottier S., Dreano S., Gattus M.T., Hitte C., Soriano N., Galibert F.;  
 RT "A 356-Kb sequence of the subtelomeric part of the MHC class I  
 RT region."  
 RL DNA Seq. 10:263-299 (1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22395763; Pubmed=14574404; DOI=10.1038/nature02055;  
 RA Shihina S., Tamiya G., Oka A., Inoko H.;  
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. AND VARIANT PRO-272.  
 RX MEDLINE=22395763; Pubmed=14574404; DOI=10.1038/nature02055;  
 RA Mungall A.J., Palmer S.C., Sims S.K., Edwards C.A., Ashurst J.L.,  
 RA Wilmshurst L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,  
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,  
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,

RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,  
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,  
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.F.,  
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,  
 RA Chapman J.C., Clark S.Y., Clark S.Y., Clee C.M., Clegg S., Cobley V.,  
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,  
 RA Cullley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,  
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,  
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,  
 RA Gilby L.M., Gilson C.J., Githero R.J., Grafham D.V., Grant M.,  
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,  
 RA Hammond S., Harley J.J., Hart E.A., Heath P.D., Heathcote R.,  
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,  
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,  
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,  
 RA Lawlor S., Leongancrlett D.A., Leversha M., Lloyd C.R., Lloyd D.M.,  
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,  
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,  
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,  
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,  
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,  
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,  
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,  
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,  
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,  
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,  
 RA Whittaker H. Wild A., Willey D.J., Wilmer T.B., Wood J.M., Wray P.W.,  
 RA Wyatt J.C., Young J., Younger R.M., Bentley D.R., Coulson A.,  
 RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;  
 RA "The DNA sequence and analysis of human chromosome 6.";  
 RL Nature 425:805-811(2003).  
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the  
 CC immune system.  
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-  
 CC microglobulin).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; X17093; CAA34947.1; -  
 CC EMBL; AF055066; AAC24827.1; -  
 CC EMBL; AF000521; BAB63337.1; -  
 CC EMBL; AL022723; CAB46623.1; -  
 CC PIR; A60384; A60384.  
 CC HSSP; Q29961; LHSA.  
 CC Genew; HGNC:4963; HLA-F.  
 CC MIM; 143110; -  
 CC GO; GO:0030106; F:MHC class I receptor activity; TAS.  
 CC InterPro; IPR007110; IG-like.  
 CC InterPro; IPR003597; IG\_c1.  
 CC InterPro; IPR003006; IG\_MHC.  
 CC InterPro; IPR001039; MHC\_I.  
 CC InterPro; IPR010579; MHC\_I\_C.  
 CC Pfam; PF00047; ig\_1.  
 CC Pfam; PF00129; MHC\_I\_1.  
 CC Pfam; PF06223; MHC\_I\_C\_1.  
 CC PRINTS; PF01639; MHCCLASSI.  
 CC ProDom; PD000050; MHC\_I\_1.  
 CC SMART; SM00407; IGc1; 1.  
 CC PROSITE; PS00835; IG LIKE; 1.  
 CC PROSITE; PS00290; IG\_MHC; 1.  
 CC Glycoprotein; MHC I; Polymorphism; Signal; Transmembrane.  
 FT SIGNAL 1 21 HUA class I histocompatibility antigen,  
 FT CHAIN 22 362 alpha chain F.  
 FT DOMAIN 22 111 Extracellular alpha-1.  
 FT DOMAIN 112 203 Extracellular alpha-2.  
 FT DOMAIN 204 295 Extracellular alpha-3.

FT DOMAIN 296 305 Connecting peptide.  
 FT TRANSMEM 306 329  
 FT DOMAIN 330 362 Cytoplasmic tail.  
 FT DISULFID 122 185 By similarity.  
 FT DISULFID 224 280 By similarity.  
 FT CARBOHYD 107 107 N-linked (GLCNAC...) (By similarity).  
 FT VARIANT 272 S -> P (in dbSNP:1736924).  
 FT /FTID=VAR\_018327.  
 SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;  
 Query Match 55.3%; Score 119; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred.No. 6.5e-117; Indels 0; Gaps 0;  
 Matches 119; Conservative 0; Mismatches 0;  
 QY 97 DGKDYISLNLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRRYLENGKET 156  
 DB 140 DGKDYISLNLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRRYLENGKET 199  
 QY 157 LORADPPKAVHHPISDHEATLRCNALGYPFAEITLTWDRGEGTQDTLVEETPAG 215  
 DB 200 LORADPPKAVHHPISDHEATLRCNALGYPFAEITLTWDRGEGTQDTLVEETPAG 258  
 RESULT 10  
 QYR27 PRELIMINARY; PRT; 362 AA.  
 AC QYR27  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Class Ib.  
 GN Name=Patr-P;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OC NCBI\_TaxId=9998;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22709134; PubMed=12799463;  
 RA Anzai T., Shima T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,  
 RA Yamagata T., Kuski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,  
 RA Yamazaki M., Tashiro H., Iwanoto C., Uehara Y., Imanishi T.,  
 RA Meyer A., Ikey K., Gojobori T., Bahram S., Inoko H.;  
 RA "Comparative sequencing of human and chimpanzee MHC class I regions  
 RT unveils insertions/deletions as the major path to genomic  
 RT divergence.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).  
 RL EMBL; AB100087; BAC78191.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR InterPro; IPR010579; MHC\_I\_C.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00129; MHC\_I\_1.  
 DR Pfam; PF06223; MHC\_I\_C\_1.  
 DR ProDom; PD000050; MHC\_I\_1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Transmembrane.  
 SQ SEQUENCE 362 AA; 40625 MW; BA5699D08181A1FF CRC64;  
 Query Match 55.3%; Score 119; DB 2; Length 362;  
 Best Local Similarity 100.0%; Pred.No. 6.5e-117; Indels 0; Gaps 0;  
 Matches 119; Conservative 0; Mismatches 0;  
 QY 97 DGKDYISLNLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRRYLENGKET 156  
 DB 140 DGKDYISLNLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRRYLENGKET 199

QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRPAG 215  
 DB 200 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRPAG 258

RESULT 11  
 BACS4915  
 ID BACS4915 PRELIMINARY; PRT; 362 AA.  
 AC BACS4915;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Major histocompatibility complex, class I, F.  
 GN HLA-F.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shima T., Oka M., Katsuyama Y., Hashimoto N., Inoko H.;  
 RT "Genome diversity in HLA: A new strategy for detection of genetic  
 RT polymorphisms in expressed genes within the HLA class III and class I  
 RT regions."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB080892; BACS4915.1; -  
 SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-117; Indels 0; Gaps 0;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWSAATVAQITQRYEAEYAEAEFFTYLEGCELELLRRYLENGKET 156  
 DB 140 DGKDYISLNEDLSRWSAATVAQITQRYEAEYAEAEFFTYLEGCELELLRRYLENGKET 199

QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRPAG 215  
 DB 200 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRPAG 258

RESULT 12  
 Q95HCO  
 ID Q95HCO PRELIMINARY; PRT; 460 AA.  
 AC Q95HCO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE HLA-F protein (Fragment).  
 GN Name=HLA-F;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatathne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Straussberg R.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC009260; AAH09260.2; -  
 DR HSP; Q29861; 1HSA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0008955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGcl; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON TER 1  
 SQ SEQUENCE 460 AA; 52263 MW; C1A0B6891978D93E CRC64;

Query Match 55.3%; Score 119; DB 2; Length 460;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-117; Indels 0; Gaps 0;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWSAATVAQITQRYEAEYAEAEFFTYLEGCELELLRRYLENGKET 156  
 DB 158 DGKDYISLNEDLSRWSAATVAQITQRYEAEYAEAEFFTYLEGCELELLRRYLENGKET 217

QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRPAG 215  
 DB 218 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRPAG 276

RESULT 13  
 Q860R0  
 ID Q860R0 PRELIMINARY; PRT; 254 AA.  
 AC Q860R0;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MHC class Ib antigen.  
 GN Name=HLA-F;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu Y., He X., Xu L., Zeng Y.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY253271; AAO86775.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0008955; P:immune response; IEA.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 SQ SEQUENCE 254 AA; 28588 MW; C81F225D409AAED2 CRC64;

Query Match 44.2%; Score 95; DB 2; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-91; Indels 0; Gaps 0;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYVDTQTLRFDSDAIPRMBPFWBQEPQWWTGYAKANAQTDVLRNLL 60

Db 44 IAVEYVDDTQFLRFPSDDAAIRMEPREPWEGEQYWEWTGYAKANAQTDRAVLRNLL 103

QY 61 RRYNSGAGSHTLQMGNGCDMGPGDGLRLRGYHQHA 95

Db 104 RRYNSGAGSHTLQMGNGCDMGPGDGLRLRGYHQHA 138

## RESULT 14

Q6ZUW0 PRELIMINARY; PRT; 349 AA.  
AC Q6ZUW0;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Hypothetical protein FL43284.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,  
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,  
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,  
RA Isogai T.,  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK125274; BAC86108.1;  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR001039; MHC I.  
DR Pfam; PF07654; CI-set; 1.  
DR DR Pfam; PF00047; IG; 1.  
DR DR Pfam; PF00129; MHC I; 1.  
DR DR Pfam; PD000050; MHC I; 1.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS0835; IG\_LIKE; 1.  
DR DR PROSITE; PS00290; IG\_MHC; 1.  
KW Transmembrane.  
SQ SEQUENCE 349 AA; 39039 MW; 5C00196F03393AA1 CRC64;

Query Match 33.0%; Score 71; DB 2; Length 349;  
Best Local Similarity 100.0%; Pred. No. 4.1e-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LLRYLENGKETLQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQIQ 204

Db 102 LLRYLENGKETLQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQIQ 161

QY 205 DTELVEITRPAG 215

Db 162 DTELVEITRPAG 172

## RESULT 15

BAC86108 PRELIMINARY; PRT; 349 AA.  
AC BAC86108;  
DT 02-MAR-2004 (TREMELrel. 27, Created)  
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)  
DE CDNA FL43284 f15, clone LYMP2000083, highly similar to HLA CLASS I  
DE HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,  
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,  
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,  
RA Isogai T.,  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK125274; BAC86108.1;  
SQ SEQUENCE 349 AA; 39039 MW; 5C00196F03393AA1 CRC64;

Query Match 33.0%; Score 71; DB 2; Length 349;  
Best Local Similarity 100.0%; Pred. No. 4.1e-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LLRYLENGKETLQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQIQ 204

Db 102 LLRYLENGKETLQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGEQIQ 161

QY 205 DTELVEITRPAG 215

Db 162 DTELVEITRPAG 172

Search completed: December 15, 2004, 18:24:23  
Job time : 112.677 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:13:46 ; Search time 21.9836 Seconds  
(without alignments)  
941.000 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 215

Sequence: 1 LAVEYVDDTQFLRFDSDAI.....QRDGEETQDTLVELTRPAG 215

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	55.3	362	2 A60384	MHC class I histoc
2	70	32.6	345	2 S07114	MHC class I histoc
3	47	21.9	348	2 S29990	histocompatibility
4	43	20.0	316	2 C37028	MHC class I histoc
5	37	17.2	365	2 JH0544	class I histocompa
6	32	14.9	255	2 I54307	MHC HLA-A30US heav
7	32	14.9	274	2 I68774	MHC HLA-B39 chain
8	32	14.9	274	2 I54463	MHC HLA-B38 chain
9	32	14.9	274	2 S24439	class I histocompa
10	32	14.9	305	2 S07115	class I histocompa
11	32	14.9	308	2 I36956	MHC class I histoc
12	32	14.9	332	2 S06424	MHC class I histoc
13	32	14.9	338	2 I56116	MHC HLA-B27-HS - h
14	32	14.9	350	2 I54308	MHC HLA B71 - huma
15	32	14.9	350	2 I68747	MHC class I lympho
16	32	14.9	354	2 S24433	class I histocompa
17	32	14.9	354	2 I59308	class I histocompa
18	32	14.9	354	2 I80166	class I histocompa
19	32	14.9	354	2 I80167	class I histocompa
20	32	14.9	354	2 I80165	class I histocompa
21	32	14.9	354	2 I80170	class I histocompa
22	32	14.9	354	2 I80168	class I histocompa
23	32	14.9	354	2 S24438	class I histocompa
24	32	14.9	354	2 S24440	class I histocompa
25	32	14.9	355	2 I80171	class I histocompa
26	32	14.9	355	2 I80169	class I histocompa
27	32	14.9	357	2 S11141	class I histocompa
28	32	14.9	358	2 S03538	class I histocompa
29	32	14.9	359	1 HLHUI2	MHC class I histoc

30	32	14.9	361	2 I54418	MHC class I histoc
31	32	14.9	362	1 HLHUI40	MHC class I histoc
32	32	14.9	362	1 HLHUI2	MHC class I histoc
33	32	14.9	362	1 HLHUI7	MHC class I histoc
34	32	14.9	362	2 JH0541	class I histocompa
35	32	14.9	362	2 JH0539	class I histocompa
36	32	14.9	362	2 JH0540	class I histocompa
37	32	14.9	362	2 I36962	MHC class I proteol
38	32	14.9	362	2 I56130	HLA-B*5401 - human
39	32	14.9	362	2 I84486	transmembrane glyc
40	32	14.9	362	2 I62042	MHC HLA-B cell sur
41	32	14.9	362	2 I37492	HLA-B alpha-chain
42	32	14.9	362	2 S52486	HLA-B protein alph
43	32	14.9	362	2 I38421	gene HLA B-1519 pr
44	32	14.9	362	2 C35997	MHC class I histoc
45	32	14.9	362	2 I56149	lymphocyte antigen

## ALIGNMENTS

### RESULT 1

A60384  
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C:Accession: A60384; J0147  
R:Kuray, D.; Epstein, H.; Holmes, N.  
Int. Immunol. 2, 531-537, 1990  
A:Title: The human class I MHC gene HLA-F is expressed in lymphocytes.  
A:Reference number: A60394, MUID:91197889; PMID:1707659  
A:Accession: A60384  
A:Molecule type: DNA  
A:Residues: 1-362 <LUR>  
A:Cross-references: UNIPROT:P30511  
R:Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.  
J. Exp. Med. 171, 1-18, 1990  
A:Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I  
A:Reference number: J0147; MUID:90111605; PMID:1668805  
A:Accession: J0147  
A:Molecule type: DNA  
A:Residues: 1-362 <GER>  
A:Cross-references: GB:X17093; NID:932223; PIDN:CAA34947.1; PID:9312407  
A:Experimental source: lymphoblastoid cell line  
C:Genetics:  
A:Gene: GDB:HLA-F  
A:Cross-references: GDB:125714  
A:Map position: 6p21.3-6p21.3  
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: glycoprotein; heterodimer; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-111/Domain: alpha-1 <AL1>  
F:78-104/Region: hypervariable  
F:112-203/Domain: alpha-2 <AL2>  
F:164-192/Region: hypervariable  
F:204-295/Domain: alpha-3 <AL3>  
F:217-282/Domain: immunoglobulin homology <IMM>  
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.3%; Score 119; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 7.8e-120; Indels 0; Gaps 0;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 97 DGKDYISLNDLRSWTAADTAQITQTFYEAEYAESEFTYLEGECLELLRRYLENGKET 156  
DB 140 DGKDYISLNDLRSWTAADTAQITQTFYEAEYAESEFTYLEGECLELLRRYLENGKET 199  
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 215  
DB 200 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 258

## RESULT 2

S07114  
MHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S07114  
R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.  
Nature 335, 268-271, 1988  
A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.  
A:Reference number: S06424; MUID:86319000; PMID:3412487  
A:Accession: S07114  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-345 <LAW>  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: Glycoprotein; membrane protein  
F:217-282/Domain: immunoglobulin homology <IMM>

Query Match 32.6%; Score 70; DB 2; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4.3e-67;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISNEDLSWTAADTVAGITQRFYAEYAEAEPTYLEGRCLELLRYLNGKET 156  
DB 140 DGKDYISNEDLSWTAADTVAGITQRFYAEYAEAEPTYLEGRCLELLRYLNGKET 199  
QY 157 LQRADPPKAAH 166  
DB 200 LQRADPPKAAH 209

## RESULT 3

S29990  
Histocompatibility antigen, HLA-F-like - rhesus macaque  
C:Species: Macaca mulatta (rhesus macaque)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S29990  
R:Bontrop, R.R.  
Submitted to the EMBL Data Library, February 1993  
A:Reference number: S29990  
A:Accession: S29990  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-348 <BON>  
C:Cross-references: UNIPROT:P33617; EMBL:Z21819; NID:G38568; PIDN:CAA79885.1; PID:G38569  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: transmembrane protein  
F:213-284/Domain: immunoglobulin homology <IMM>

Query Match 21.9%; Score 47; DB 2; Length 348;  
Best Local Similarity 100.0%; Pred. No. 2.5e-42;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ITQRFYAEYAEAEPTYLEGRCLELLRYLNGKETLQRAADPPKAAH 166  
DB 165 ITQRFYAEYAEAEPTYLEGRCLELLRYLNGKETLQRAADPPKAAH 211

## RESULT 4

C37028  
MHC class I histocompatibility antigen HLA-C (clone 9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1992 #sequence\_revision 30-Jan-1993 #text\_change 09-Jul-2004  
C:Accession: C37028  
R:Cianetti, L.; Testa, U.; Scotto, L.; La Valle, R.; Simeone, A.; Boccoli, G.; Giannella  
Immunogenetics 29, 80-91, 1989  
A:Title: Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of  
A:Reference number: A37028; MUID:89122144; PMID:2914713  
A:Accession: C37028  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-316 <CIA>  
A:Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q29987; UNIPROT:Q9MY34; UNIPROT:O19677; UNIF

## C:Genetics:

A:Gene: GDB:HLA-C  
A:Cross-references: GDB:119311; OMIM:142840  
A:Map position: 6p21.3-6p21.3  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:170-235/Domain: immunoglobulin homology <IMM>

Query Match 20.0%; Score 43; DB 2; Length 316;  
Best Local Similarity 100.0%; Pred. No. 4.6e-38;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 SDHEATLRCWALGFYPAEITLTWQDGBEQTDTELVEVPAG 215  
DB 169 SDHEATLRCWALGFYPAEITLTWQDGBEQTDTELVEVPAG 211

## RESULT 5

JH0544  
class I histocompatibility antigen heavy chain precursor - lowland gorilla  
C:Species: Gorilla gorilla gorilla (lowland gorilla)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: JH0544; JH0543  
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.  
J. Exp. Med. 174, 1491-1509, 1991  
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human a1  
A:Reference number: JH0534; MUID:92078860; PMID:11744581  
A:Accession: JH0544  
A:Molecule type: DNA  
A:Residues: 1-365 <LAW>  
A:Cross-references: UNIPROT:P30383; EMBL:X60250; NID:G22878; PIDN:CAA42802.1; PID:G22879  
A:Experimental source: EBV-transformed B cell  
A:Note: Gogo-C0102  
A:Accession: JH0543  
A:Molecule type: DNA  
A:Residues: 1-319, 'S', 321-365 <LA2>  
A:Cross-references: EMBL:X60252  
A:Experimental source: EBV-transformed B cell  
A:Note: Gogo-C0101  
A:Note: the authors translated the codon AGT for residue 320 as Val  
C:Genetics: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-365/Product: class I histocompatibility antigen heavy chain #status predicted <CLA>  
F:25-114/Domain: alpha-1 <AL1>  
F:115-206/Domain: alpha-2 <AL2>  
F:207-298/Domain: alpha-3 <AL3>  
F:220-285/Domain: immunoglobulin homology <IMM>  
F:299-365/Domain: intracellular #status predicted <INT>

Query Match 17.2%; Score 37; DB 2; Length 365;  
Best Local Similarity 100.0%; Pred. No. 1.5e-31;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGBEQTD 205  
DB 215 HHPISDHEATLRCWALGFYPAEITLTWQDGBEQTD 251

## RESULT 6

I54307  
MHC HLA-A30JS heavy chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C:Accession: I54307  
R:Choo, S.Y.; Starling, G.C.; Anasetti, C.; Hansen, J.A.  
Hum. Immunol. 36, 20-26, 1993  
A:Title: Selection of an unrelated donor for marrow transplantation facilitated by the m  
A:Reference number: I54307; MUID:93209813; PMID:8458735  
A:Accession: I54307  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-255 <RES>  
 A:Cross-references: GB:M93657; NID:g184155; PIDN:AAA58650.1; PID:g553335  
 C:Genetics:  
 A:Gene: HLA-A30J5  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 14.9%; Score 32; DB 2; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 7  
 I68774  
 MHC HLA-B39 chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
 C:Accession: I68774  
 R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.  
 Immunogenetics 30, 200-207, 1989  
 A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificity  
 A:Reference number: I54463; MUID:89379286; PMID:2777338  
 A:Accession: I68774  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-274 <RES>  
 A:Cross-references: UNIPROT:Q29937; GB:M29865; NID:g187676; PIDN:AAA36223.1; PID:g187677  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:196-261/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 8  
 I54463  
 MHC HLA-B38 chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
 C:Accession: I54463  
 R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.  
 Immunogenetics 30, 200-207, 1989  
 A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificity  
 A:Reference number: I54463; MUID:89379286; PMID:2777338  
 A:Accession: I54463  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-274 <RES>  
 A:Cross-references: UNIPROT:Q95365; GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:196-261/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 9  
 S24439  
 class I histocompatibility antigen HLA-B-3901 - human (fragment)  
 C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C:Accession: S24439  
 R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe  
 Nature 357, 323-333, 1992  
 A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate  
 A:Reference number: S24027; MUID:92269956; PMID:1589035  
 A:Accession: S24439  
 A:Molecule type: mRNA  
 A:Residues: 1-274 <MAT>  
 A:Cross-references: UNIPROT:Q96DW9; UNIPROT:Q8WLS2; UNIPROT:O19790; UNIPROT:Q95351; UNIP  
 PROT:Q78218; UNIPROT:Q29653; UNIPROT:Q29657; UNIPROT:Q29654; UNIPROT:Q29655; UNIPROT:Q08  
 U994; UNIPROT:Q951E7; UNIPROT:Q95346  
 C:Genetics:  
 A:Gene: HLA-B-3901  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 C:Keywords: Glycoprotein  
 F:1-374/Product: Class I histocompatibility antigen HLA-B-3901 #status predicted <MAT>  
 F:1-90/Domain: alpha-1 #status predicted <EX1>  
 F:91-182/Domain: alpha-2 #status predicted <EX2>  
 F:196-261/Domain: immunoglobulin homology <IMM>  
 F:186-Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:101-164,203-259/Disulfide bonds: #status predicted

Query Match 14.9%; Score 32; DB 2; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 10  
 S07115  
 class I histocompatibility antigen Ch18 alpha chain - chimpanzee (fragment)  
 N:Alternate names: MHC Ch18 chain  
 C:Species: Pan troglodytes (Chimpanzee)  
 C:Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
 C:Accession: S07115; I36960  
 R:Lawlor, D.A.; Ward, F.B.; Ennis, P.D.; Jackson, A.P.; Parham, P.  
 Nature 335, 268-271, 1988  
 A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.  
 A:Reference number: S06424; MUID:88319000; PMID:3412487  
 A:Accession: S07115  
 A:Molecule type: mRNA  
 A:Residues: 1-305 <LAW>  
 A:Cross-references: UNIPROT:Q30991  
 R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
 J. Immunol. 142, 3937-3950, 1989  
 A:Title: Diversity and diversification of HLA-A, B, C alleles.  
 A:Reference number: I36956; MUID:89235215; PMID:2715640  
 A:Accession: I36960  
 A:Molecule type: mRNA  
 A:Residues: 1-305 <RES>  
 A:Cross-references: GB:M24048; NID:g176820; PIDN:AAA35427.1; PID:g176821  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 C:Keywords: Glycoprotein; membrane protein  
 F:58-149/Domain: alpha-2 #status predicted <EX2>  
 F:163-228/Domain: immunoglobulin homology <IMM>  
 F:250-274/Domain: transmembrane #status predicted <TM>  
 F:275-305/Domain: intracellular #status predicted <INT>  
 F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:168-131,170-226/Disulfide bonds: #status predicted

Query Match 14.9%; Score 32; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 DB 158 HHPISDHEATLRCWALGFYPAEITLTWQDGE 189

## RESULT 11

I36956  
 MHC class I chain - chimpanzee (fragment)  
 C:Species: Pan troglodytes (chimpanzee)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I36956  
 R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
 J. Immunol. 142, 3937-3950, 1989  
 A:Title: Diversity and diversification of HLA-A,B,C alleles.  
 A:Reference number: I36956; MUID:89235215; PMID:2715640  
 A:Accession: I36956  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <RES>  
 A:Cross-references: UNIPROT:O19357; GB:M24044; NID:G176812; PIDN:AAA35423.1; PID:G176813  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:165-231/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 308;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
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 DB 161 HHPISDHEATLRCWALGFYPAEITLTWQDGE 192

## RESULT 12

S06424  
 MHC class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee  
 A:Alternate names: MHC Ch1a chain  
 C:Species: Pan troglodytes (chimpanzee)  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C:Accession: S06424; I36959  
 R:Lawlor, D.A.; Ward, F.B.; Ennis, P.D.; Jackson, A.P.; Parham, P.  
 Nature 335, 268-271, 1988  
 A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.  
 A:Reference number: S06424; MUID:88319000; PMID:3412487  
 A:Accession: S06424  
 A:Molecule type: mRNA  
 A:Residues: 1-332 <LAW>  
 A:Cross-references: UNIPROT:Q30990  
 R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
 J. Immunol. 142, 3937-3950, 1989  
 A:Title: Diversity and diversification of HLA-A,B,C alleles.  
 A:Reference number: I36956; MUID:89235215; PMID:2715640  
 A:Accession: I36959  
 A:Molecule type: mRNA  
 A:Residues: 1-332 <RES>  
 A:Cross-references: GB:M24047; NID:G176818; PIDN:AAA35426.1; PID:G553155  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 C:Keywords: glycoprotein; membrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-114/Domain: alpha-1 #status predicted <EX1>  
 F:115-206/Domain: alpha-2 #status predicted <EX2>  
 F:220-285/Domain: immunoglobulin homology <IMM>  
 F:307-331/Domain: transmembrane #status predicted <TMW>  
 F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:125-168,227-283/Disulfide bonds: #status predicted

Query Match 14.9%; Score 32; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 |||||  
 DB 215 HHPISDHEATLRCWALGFYPAEITLTWQDGE 246

## RESULT 13

I56116  
 MHC HLA-B\*27-HS - human (fragment)  
 C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I56116  
 R:Choo, S.Y.; Fan, L.A.; Hansen, J.A.  
 J. Immunol. 147, 174-180, 1991  
 A:Title: A novel HLA-B\*27 allele maps B27 allotypicity to the region around position 70  
 A:Reference number: I56116; MUID:91268545; PMID:1711072  
 A:Accession: I56116  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-338 <RES>  
 A:Cross-references: UNIPROT:P03989; GB:M62852; NID:G187760; PIDN:AAA59647.1; PID:G187761  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:196-261/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 338;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 |||||  
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

## RESULT 14

I54308  
 MHC HLA B\*71 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I54308  
 R:Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.  
 Hum. Immunol. 37, 192-194, 1993  
 A:Title: Molecular characterization of HLA-B\*71 from an African American individual.  
 A:Reference number: I54308; MUID:94064392; PMID:8244782  
 A:Accession: I54308  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-350 <RES>  
 A:Cross-references: UNIPROT:Q08173; GB:L07950; NID:G307236; PIDN:AAA59683.1; PID:G307237  
 C:Genetics:  
 A:Gene: GDB:HLA-B  
 A:Cross-references: GDB:120048; OMIM:142830  
 A:Map position: 6p21.3-6p21.3  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-26;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200  
 |||||  
 DB 215 HHPISDHEATLRCWALGFYPAEITLTWQDGE 246

## RESULT 15

I68747  
 MHC class I lymphocyte antigen - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
 C:Accession: I68747  
 R:Phila, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, B.H.  
 Immunogenetics 29, 297-307, 1989  
 A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B\*8  
 A:Reference number: I54457; MUID:89233295; PMID:2714852  
 A:Accession: I68747  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-350 <RES>  
 A:Cross-references: UNIPROT:O19691; GB:M28204; NID:G576472; PIDN:AAA53257.1; PID:G576473  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:208-273/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 350;

Best Local Similarity 100.0%; Pred. No. 3.6e-26;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFYPAEITLTLTWORGE 200  
Db 203 HHPISDHEATLRCWALGFYPAEITLTLTWORGE 234

Search completed: December 15, 2004, 18:25:18  
Job time : 22.9836 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:24:34 ; Search time 87.4949 Seconds  
(without alignments)  
877.689 Million cell updates/sec

Title: US-09-819-371-6  
Perfect score: 215  
Sequence: 1 IAVEYVDDTQFLRDSDAAI.....QRDGEQTQDTLVETRPAG 215

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1585576 seqs, 357178320 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*  
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16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pap.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215	100.0	215	11	US-09-819-371-6
2	119	55.3	271	11	US-09-819-371-6
3	119	55.3	274	11	US-09-819-371-5
4	119	55.3	362	14	US-10-257-021-82
5	119	55.3	442	16	US-10-408-765A-1887
6	95	44.2	362	11	US-09-819-371-4
7	55	25.6	96	14	US-10-029-386-30718
8	52	24.2	186	15	US-10-264-049-4063
9	32	14.9	91	9	US-09-864-761-35461
10	32	14.9	110	9	US-09-796-692-799
11	32	14.9	110	9	US-09-796-692-799
12	32	14.9	110	14	US-10-040-862-799
13	32	14.9	110	14	US-10-040-862-2139

14	14.9	110	15	US-10-057-475B-799	Sequence 799, Appl
15	14.9	110	15	US-10-057-475B-2139	Sequence 2139, Ap
16	14.9	110	15	US-10-154-884B-799	Sequence 799, Appl
17	14.9	110	15	US-10-154-884B-2139	Sequence 2139, Ap
18	14.9	110	16	US-10-764-324-799	Sequence 799, Appl
19	14.9	110	16	US-10-764-324-2139	Sequence 2139, Ap
20	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
21	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
22	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
23	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
24	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
25	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
26	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
27	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
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29	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
30	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
31	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
32	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
33	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
34	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
35	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
36	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
37	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
38	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
39	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
40	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
41	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
42	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
43	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
44	14.9	136	15	US-10-262-839-48	Sequence 48, Appl
45	14.9	136	15	US-10-262-839-48	Sequence 48, Appl

## ALIGNMENTS

RESULT 1  
US-09-819-371-6  
; Sequence 6, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-6

Query Match 100.0%; Score 215; DB 11; Length 215;  
Best Local Similarity 100.0%; Pred. No. 6.5e-203;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	IAVEYVDDTQFLRDSDAAI	PRMEPEPEVQEGPGYEWTTGYAKANAQTDRLVALNLL	60
DB	1	IAVEYVDDTQFLRDSDAAI	PRMEPEPEVQEGPGYEWTTGYAKANAQTDRLVALNLL	60
QY	61	RRYNQSEAGSHLTQGMNCGDMG	DGRLRGYHQHAWDGKDYISLNEEDLSRWTAADTVAQI	120
DB	61	RRYNQSEAGSHLTQGMNCGDMG	DGRLRGYHQHAWDGKDYISLNEEDLSRWTAADTVAQI	120
QY	121	TORFYEEVABEFRTYLGECLEL	RLRYLNGKETLQADPPKAVHHPISDHEATLR	180
DB	121	TORFYEEVABEFRTYLGECLEL	RLRYLNGKETLQADPPKAVHHPISDHEATLR	180
QY	181	CWALGFYFABITITWDRDGEQ	DTLVETRPAG 215	

Db 181 CWALGFYPAEITLTWQDGEQQTDTLVETRPAG 215  
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## RESULT 2

US-09-925-301-1431  
; Sequence 1431, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1431  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1431

Query Match 55.3%; Score 119; DB 9; Length 271;

Best Local Similarity 100.0%; Pred. No. 2e-108;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156  
Db 146 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 205  
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 215  
Db 206 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 264

## RESULT 3

US-09-819-371-5  
; Sequence 5, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-5

Query Match 55.3%; Score 119; DB 11; Length 274;

Best Local Similarity 100.0%; Pred. No. 2e-108;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156  
Db 119 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 178  
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 215  
Db 179 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 237

## RESULT 4

US-10-257-021-82

; Sequence 82, Application US/10257021  
; Publication No. US20030211498A1  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Patrice J.  
; APPLICANT: Sherman-Baust, Cheryl A.  
; APPLICANT: Pizer, Ellen S.  
; APPLICANT: Hough, Colleen D.  
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
; FILE REFERENCE: 14014.0369U2  
; CURRENT APPLICATION NUMBER: US/10/257,021  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/10947  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/194,336  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-257-021-82

Query Match 55.3%; Score 119; DB 14; Length 362;

Best Local Similarity 100.0%; Pred. No. 2.5e-108;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156  
Db 140 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 199  
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 215  
Db 200 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 258

## RESULT 5

US-10-408-765A-1887  
; Sequence 1887, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Robin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1887  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1887

Query Match 55.3%; Score 119; DB 16; Length 442;

Best Local Similarity 100.0%; Pred. No. 3e-108;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156  
Db 140 DGKDYISLNEDLSWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 199  
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 215  
Db 200 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVETRPAG 258

## RESULT 6

US-09-819-371-4 ; Sequence 4, Application US/09819371 ; Publication No. US20040053344A1 ; GENERAL INFORMATION:

```

; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-4

```

Query Match	44.2%;	Score 95;	DB 11;	Length 362;
Best Local Similarity	100.0%;	Pred. No. 1e-84;		
Matches	95;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QV 1 IAVEYVDDTOFLRFDSDAI PRMEPREPWEOEGPOYNEWTTGYAKANACTDRVAENLL 60

44 IAVEYVDDTQFLRFDSDAAIPRMEPRBPWEQEGPQYNEWTTGYAKANAQTDVALRNLL 103

QV 61 RRYNOSEAGSHTLOGMNGCDMGPDRLLRGYHOHA 95

104 RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHA 138

## RESULT 7

US-10-029-386-30718  
; Sequence 30718, Application US/10029386  
; Publication No. US20030194704A1

```

GENERAL INFORMATION: US069878A
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOmica-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 30718
LENGTH: 96
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```

;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; OTHER INFORMATION: MAP TO CHR6.1
;
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
;
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
;
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718

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Query Match      25.6%; Score 55; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.5e-46;
Matches 55: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OV 161 DPPKAHVAAHPISDHEATLRCAWALGEYPAETTTIWORDGEEOTODTEI.VETRRPAG 215

[illegible]

## RESULT 8

US-10-264-049-4063  
; Sequence 4063, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:

**GENERAL INFORMATION:**

```

1  APPLICANT: Birse et al.
2  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
3  FILE REFERENCE: FA133P1
4  CURRENT APPLICATION NUMBER: US/10/264,049
5  CURRENT FILING DATE: 2002-10-04
6  PRIOR APPLICATION NUMBER: PCT/US01/18569
7  PRIOR FILING DATE: 2001-06-07
8  PRIOR APPLICATION NUMBER: US 60/209,467
9  PRIOR FILING DATE: 2000-06-07
10 NUMBER OF SEQ ID NOS: 4360
11 SOFTWARE: PatentIn Ver. 3.1
12 SEQ ID NO 4063
13 LENGTH: 186
14 TYPE: PRT
15 ORGANISM: Homo sapiens
16 FEATURE:
17 NAME/KEY: MISC_FEATURE
18 LOCATION: (75)_FEATURE
19 OTHER INFORMATION: Xaa equals any of the twenty naturally
20 FEATURE:
21 NAME/KEY: MISC_FEATURE
22 LOCATION: (77)_
23 OTHER INFORMATION: Xaa equals any of the twenty naturally
24 FEATURE:
25 NAME/KEY: MISC_FEATURE
26 LOCATION: (85)_
27 OTHER INFORMATION: Xaa equals any of the twenty naturally
28 FEATURE:
29 NAME/KEY: MISC_FEATURE
30 LOCATION: (107)
31 OTHER INFORMATION: Xaa equals any of the twenty naturally
32 FEATURE:
33 NAME/KEY: MISC_FEATURE
34 LOCATION: (123)
35 OTHER INFORMATION: Xaa equals any of the twenty naturally
36 FEATURE:
37 NAME/KEY: MISC_FEATURE
38 LOCATION: (124)
39 OTHER INFORMATION: Xaa equals any of the twenty naturally
40 FEATURE:
41 NAME/KEY: MISC_FEATURE
42 LOCATION: (136)
43 OTHER INFORMATION: Xaa equals any of the twenty naturally
44 FEATURE:
45 NAME/KEY: MISC_FEATURE
46 LOCATION: (148)
47 OTHER INFORMATION: Xaa equals any of the twenty naturally
48 FEATURE:
49 NAME/KEY: MISC_FEATURE
50 LOCATION: (163)
51 OTHER INFORMATION: Xaa equals any of the twenty naturally
52 FEATURE:
53 NAME/KEY: MISC_FEATURE
54 LOCATION: (174)
55 OTHER INFORMATION: Xaa equals any of the twenty naturally
56 FEATURE:
57 NAME/KEY: MISC_FEATURE
58 LOCATION: (175)
59 OTHER INFORMATION: Xaa equals any of the twenty naturally
60 FEATURE:
61 NAME/KEY: MISC_FEATURE
62 LOCATION: (176)
63 OTHER INFORMATION: Xaa equals any of the twenty naturally
64 FEATURE:
65 NAME/KEY: MISC_FEATURE
66 LOCATION: (180)
67 OTHER INFORMATION: Xaa equals any of the twenty naturally
68 US-10-264,049-4063

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Query Match      24.2%; Score 52; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 52: Conservative 0; Mismatches 0; Indels
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2000 Local Primary	100.00%	100.00%	100.00%	100.00%
Matches	52:	Conservative	0:	Mismatches
0:	Indels	0:	Gaps	0:



```
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077, 001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2139

Query Match      14.9%; Score 32; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
Db      67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 12
US-10-040-862-799
; Sequence 799, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
```

```
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 799
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-799

Query Match      14.9%; Score 32; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
Db      67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 13
US-10-040-862-2139
; Sequence 2139, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
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; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-2139

```

```

Query Match      14.9%; Score 32; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
      |||||||
Db 67 HHPISDHEATLRCWALGFYPAEITLTWQDGE 98

```

```

RESULT 14
US-10-057-475B-799
; Sequence 799, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10379
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 799
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-799

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```

Query Match      14.9%; Score 32; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
      |||||||
Db 67 HHPISDHEATLRCWALGFYPAEITLTWQDGE 98

```

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RESULT 15
US-10-057-475B-2139
; Sequence 2139, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10379
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-2139

```

```

Query Match      14.9%; Score 32; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
      |||||||
Db 67 HHPISDHEATLRCWALGFYPAEITLTWQDGE 98

```

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Search completed: December 15, 2004, 18:41:49
Job time : 88.4949 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 18:14:01 ; Search time 24.182 Seconds  
(without alignments)  
589.627 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 215

Sequence: 1 IAVEYVDDTQFLRFDSDAAI.....CRDGEHQDTQLVETRPAG 215

Scoring table:

OLIGO

Gapop 60.0 ; Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	35.8	120	4	US-09-513-999C-4290
2	32	14.9	274	1	US-08-222-851-1
3	17	7.9	184	3	US-09-153-586-21
4	16	7.4	117	2	US-08-406-057-9
5	16	7.4	117	2	US-08-958-316-8
6	16	7.4	145	2	US-08-406-057-8
7	16	7.4	145	3	US-08-958-316-8
8	16	7.4	361	3	US-08-652-265-22
9	16	7.4	361	3	US-08-834-497A-22
10	16	7.4	361	3	US-09-503-444A-22
11	15	7.0	92	4	US-09-673-809-25
12	15	7.0	182	1	US-08-127-954-135
13	15	7.0	182	1	US-08-127-954-151
14	15	7.0	274	2	US-08-484-905-105
15	15	7.0	274	2	US-08-484-905-106
16	15	7.0	274	2	US-08-484-905-107
17	15	7.0	274	2	US-08-484-905-108
18	15	7.0	274	3	US-08-481-985B-105
19	15	7.0	274	3	US-08-481-985B-106
20	15	7.0	274	3	US-08-481-985B-107
21	15	7.0	274	3	US-08-481-985B-108
22	15	7.0	274	3	US-08-370-476-105
23	15	7.0	274	3	US-08-370-476-106
24	15	7.0	274	3	US-08-370-476-107
25	15	7.0	274	3	US-08-370-476-108
26	15	7.0	341	3	US-08-890-719-38
27	15	7.0	365	2	US-08-484-905-97

Sequence 98, Appl  
Sequence 99, Appl  
Sequence 100, Appl  
Sequence 101, Appl  
Sequence 102, Appl  
Sequence 103, Appl  
Sequence 104, Appl  
Sequence 97, Appl  
Sequence 98, Appl  
Sequence 99, Appl  
Sequence 100, Appl  
Sequence 101, Appl  
Sequence 102, Appl  
Sequence 103, Appl  
Sequence 104, Appl  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 97, Appl

365 2 US-08-484-905-98  
365 2 US-08-484-905-99  
365 2 US-08-484-905-100  
365 2 US-08-484-905-101  
365 2 US-08-484-905-102  
365 2 US-08-484-905-103  
365 2 US-08-484-905-104  
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365 3 US-08-481-985B-101  
365 3 US-08-481-985B-102  
365 3 US-08-481-985B-103  
365 3 US-08-481-985B-104  
365 3 US-08-652-265-23  
365 3 US-08-834-497A-23  
365 3 US-08-370-476-97

#### ALIGNMENTS

RESULT 1  
US-09-513-999C-4290  
; Sequence 4290, Application US/09513999C  
; Patent No. 6783361  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783361  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4290  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -17...-1  
; OTHER INFORMATION: score 9.3  
; OTHER INFORMATION: seq SLALLSGALALT/DT  
US-09-513-999C-4290

Query Match 35.8%; Score 77; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.8e-69;  
Matches 77; Conservative 0; Mismatches 0; Gaps 0;  
QY 1 IAVEYVDDTQFLRFDSDAAI PRMPEPWEQSGPQWETTCYAKANAQTDRVALRNL 60  
DB 44 IAVEYVDDTQFLRFDSDAAI PRMPEPWEQSGPQWETTCYAKANAQTDRVALRNL 103  
QY 61 RRYNQSEAGSHTLQGMN 77  
DB 104 RRYNQSEAGSHTLQGMN 120

RESULT 2  
US-08-222-851-1  
; Sequence 1, Application US/08222851  
; Patent No. 5723128  
; GENERAL INFORMATION:  
; APPLICANT: CLAYBERGER, CAROL A.  
; APPLICANT: KRENSKY, ALAN M.  
; APPLICANT: PARHAM, PETER  
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")

;; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES

;; NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: MORRISON & FOERSTER

;; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500

;; CITY: WASHINGTON

;; STATE: DC

;; COUNTRY: USA

;; ZIP: 20006-1812

;; COMPUTER READABLE FORM:

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/222,851

;; FILING DATE: 05-APR-1994

;; CLASSIFICATION: 424

;; ATTORNEY/AGENT INFORMATION:

;; NAME: MILLMAN, ROBERT A.

;; REGISTRATION NUMBER: 36,217

;; REFERENCE/DOCKET NUMBER: 28600-20200.22

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202) 887-1500

;; TELEFAX: (202) 494-0792

;; TELEX: 90-4030 MRSNFORESWH

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 274 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; US-09-222-851-1

Query Match 14.9%; Score 32; DB 1; Length 274;

Best Local Similarity 100.0%; Pred. No. 5.7e-24; Indels 0; Gaps 0;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATRCWALGFYPAEITLTWQDGE 200

Db 191 HHPISDHEATRCWALGFYPAEITLTWQDGE 222

RESULT 3

US-09-153-586-21

;; Sequence 21, Application US/09153586A

;; Patent No. 6270772

;; GENERAL INFORMATION:

;; APPLICANT: Burrows et al.

;; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of

;; FILE REFERENCE: 48823

;; CURRENT APPLICATION NUMBER: US/09/153,586A

;; CURRENT FILING DATE: 1998-09-15

;; EARLIER FILING DATE: 1997-09-16

;; EARLIER FILING DATE: 1997-09-16

;; EARLIER FILING DATE: 1997-10-10

;; NUMBER OF SEQ ID NOS: 30

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 21

;; LENGTH: 184

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; US-09-153-586-21

Query Match 7.9%; Score 17; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 3.9e-09; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 LRRYLENGKETLQRADP 162

Db 168 LRRYLENGKETLQRADP 184

RESULT 4

US-08-406-057-9

;; Sequence 9, Application US/08406057

;; Patent No. 5856442

;; GENERAL INFORMATION:

;; APPLICANT: CAROSELLA, EDGARDO D

;; APPLICANT: MOREAU, PHILIPPE

;; APPLICANT: GLUCKMAN, ELIANE

;; APPLICANT: KIRSZENBAUM, MAREK

;; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G

;; NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

;; CITY: ARLINGTON

;; STATE: VIRGINIA

;; COUNTRY: USA

;; ZIP: 2202

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Tape

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/406,057

;; FILING DATE: 17-MAR-1995

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: PR 94 03179

;; FILING DATE: 18-MAR-1994

;; ATTORNEY/AGENT INFORMATION:

;; NAME: OBLON, NORVAN F

;; REGISTRATION NUMBER: 24,618

;; REFERENCE/DOCKET NUMBER: 846-331-0

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (703) 413-3000

;; TELEFAX: (703) 413-2220

;; TELEX: 248855 OPAT UR

;; INFORMATION FOR SEQ ID NO: 9:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 117 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; US-08-406-057-9

Query Match 7.4%; Score 16; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.6e-08; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 EATLRWALGFYPAEI 191

Db 20 EATLRWALGFYPAEI 35

RESULT 5

US-08-958-316-9

;; Sequence 9, Application US/08958316

;; Patent No. 6291659

;; GENERAL INFORMATION:

;; APPLICANT: CAROSELLA, EDGARDO D

;; APPLICANT: MOREAU, PHILIPPE

;; APPLICANT: GLUCKMAN, ELIANE

;; APPLICANT: KIRSZENBAUM, MAREK

;; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G

;; NUMBER OF SEQUENCES: 17

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 2202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958,316  
FILING DATE: 27-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 0846-0437-0  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-958-316-9

Query Match 7.4% Score 16; DB 3; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.6e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
Db 20 EATLRCWALGFYPAEI 35

RESULT 6  
US-08-406-057-8  
Sequence 8, Application US/08406057  
Patent No. 5856442  
GENERAL INFORMATION:  
APPLICANT: CAROSELLA, EDGARDO D  
APPLICANT: MOREAU, PHILIPPE  
APPLICANT: GLUCKMAN, ELIJANE  
APPLICANT: KIRSZENBAUM, MAREK  
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 2202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,057  
FILING DATE: 17-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: FR 94 03179

FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 846-331-0  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-406-057-8

Query Match 7.4% Score 16; DB 2; Length 145;  
Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
Db 48 EATLRCWALGFYPAEI 63

RESULT 7  
US-08-958-316-8  
Sequence 8, Application US/08958316  
Patent No. 6291659  
GENERAL INFORMATION:  
APPLICANT: CAROSELLA, EDGARDO D  
APPLICANT: MOREAU, PHILIPPE  
APPLICANT: GLUCKMAN, ELIJANE  
APPLICANT: KIRSZENBAUM, MAREK  
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 2202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958,316  
FILING DATE: 27-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 0846-0437-0  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-958-316-8

Query Match 7.4%; Score 16; DB 3; Length 145;  
Best Local Similarity 100.0%; Pred. No. 3.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
|||||  
DB 48 EATLRCWALGFYPAEI 63

## RESULT 8

US-08-652-265-22  
; Sequence 22, Application US/08652265

; Patent No. 6025130

; GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.

; APPLICANT: Drayna, Dennis T.

; APPLICANT: Feder, John N.

; APPLICANT: Gnirke, Andreas

; APPLICANT: Ruddy, David

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Hereditary Hemochromatosis Gene

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,265

; FILING DATE: 23-MAY-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 17957-000500

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 361 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..361

; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"

US-08-652-265-22

Query Match 7.4%; Score 16; DB 3; Length 361;  
Best Local Similarity 100.0%; Pred. No. 7.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
|||||  
DB 222 EATLRCWALGFYPAEI 237

## RESULT 9

US-08-934-497A-22

; Sequence 22, Application US/08934497A

; Patent No. 6140305

; GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.

; APPLICANT: Drayna, Dennis T.

; APPLICANT: Feder, John N.

; APPLICANT: Gnirke, Andreas

; APPLICANT: Ruddy, David

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS

; NUMBER OF SEQUENCES: 76

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,497A

; FILING DATE: 04-APR-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/652,265

; FILING DATE: 23-MAY-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/632,673

; FILING DATE: 16-APR-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,912

; FILING DATE: 04-APR-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Poissant, Brian M.

; REGISTRATION NUMBER: 28,462

; REFERENCE/DOCKET NUMBER: 8907-0056-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 361 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..361

; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"

US-08-834-497A-22

Query Match 7.4%; Score 16; DB 3; Length 361;  
Best Local Similarity 100.0%; Pred. No. 7.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
|||||  
DB 222 EATLRCWALGFYPAEI 237

## RESULT 10

US-09-503-444A-22

; Sequence 22, Application US/09503444A

; Patent No. 6228594

GENERAL INFORMATION:  
APPLICANT: Thomas, Winston J.  
APPLICANT: Drayna, Dennis T.  
APPLICANT: Feder, John N.  
APPLICANT: Gnirke, Andreas  
APPLICANT: Guddy, David  
APPLICANT: Ruddy, David  
APPLICANT: Teuchihashi, Zenta  
APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect Version 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/503,444A  
FILING DATE: 14-Feb-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/652,265  
FILING DATE: 23-May-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/632,673  
FILING DATE: 16-Apr-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,912  
FILING DATE: 04-Apr-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0088-999  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 361 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..361  
OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"  
US-09-503-444A-22

Query Match 7.4%; Score 16; DB 3; Length 361;  
Best Local Similarity 100.0%; Pred. No. 7.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAP1 191  
DB 222 EATLRCWALGFYPAP1 237

RESULT 11  
US-09-673-809-25  
Sequence 25, Application US/09673809  
Patent No. 6528261  
GENERAL INFORMATION:  
APPLICANT: INNOGENETICS N.V.  
TITLE OF INVENTION: Method for typing of HLA alleles.  
FILE REFERENCE: PCT99.86.HLA

CURRENT APPLICATION NUMBER: US/09/673,809  
CURRENT FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 98870088.6  
PRIOR FILING DATE: 1998-04-20  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 25  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-673-809-25  
Query Match 7.0%; Score 15; DB 4; Length 92;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 146 LRRYLENGKETLQRA 160  
DB 78 LRRYLENGKETLQRA 92  
RESULT 12  
US-08-127-954-135  
Sequence 135, Application US/08127954  
Patent No. 5451512  
GENERAL INFORMATION:  
APPLICANT: Apple, Raymond J.  
APPLICANT: Bugawan, Teodorica L.  
APPLICANT: Erlich, Henry A.  
TITLE OF INVENTION: Methods and Reagents for HLA Class I A  
TITLE OF INVENTION: Locus DNA Typing  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingeland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,954  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 8873  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 182 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-127-954-135

Query Match 7.0%; Score 15; DB 1; Length 182;  
Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 146 LRRYLENGKETLQRA 160  
DB 168 LRRYLENGKETLQRA 182

```

RESULT 13
US-08-127-954-151
; Sequence 151, Application US/08127954
; Patent No. 5451512
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; TITLE OF INVENTION: Methods and Reagents for HLA Class I A
; TITLE OF INVENTION: Locus DNA Typing
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8873
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-127-954-151

Query Match      7.0%; Score 15; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      146 LRRYLENGKETLQRA 160
Db      168 LRRYLENGKETLQRA 182

```

```

RESULT 14
US-08-484-905-105
; Sequence 105, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473

```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-105

Query Match      7.0%; Score 15; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      186 FYPAEITLTWQDGE 200
Db      208 FYPAEITLTWQDGE 222

```

```

RESULT 15
US-08-484-905-106
; Sequence 106, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473

```

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; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-106

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Query Match      7.0%; Score 15; DB 2; Length 274;
Best Local Similarity 100.0%; Pred.No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      186 FYPAEITLTWORDGE 200
          |||||
Db      208 FYPAEITLTWORDGE 222

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Search completed: December 15, 2004, 18:26:19  
 Job time : 25.182 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:00 / Search time 95.8487 Seconds  
(without alignments)  
804.673 Million cell updates/sec

Title: US-09-819-371-6  
Perfect score: 215  
Sequence: 1 LAVEYVDITQLRFDSDAAI.....QRDGEQTQDTLVELTRPAG 215

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 2002273 seqs, 358729299 residues  
Word size: 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A\_Geneseq\_23Sep04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	55.3	215	4	AAG64619 Human can
2	119	55.3	215	7	ADP55589
3	119	55.3	271	3	AAB43986 Human can
4	119	55.3	274	4	AAG64618 Human can
5	119	55.3	274	7	ADP55588
6	119	55.3	362	4	AAG64617 Human can
7	119	55.3	362	4	AB350296 HLA-Cw ov
8	119	55.3	362	7	ADP55587
9	119	55.3	362	8	ADJ75372 Marker ge
10	119	55.3	362	8	ADP12500 Protein e
11	119	55.3	442	7	ADJ70081 Human hea
12	119	55.3	677	4	ABG26726 Novel hum
13	77	35.8	120	3	AG000209 Human sec
14	55	25.6	96	8	ABO57084 Human gen
15	52	24.2	186	5	ABP42931 Human ova
16	32	14.9	91	4	AA115751 Peptide #
17	32	14.9	91	4	AA115751 Peptide #
18	32	14.9	91	4	AB34748 Peptide #
19	32	14.9	91	4	AB28260 Peptide #
20	32	14.9	91	4	AB22570 Peptide #
21	32	14.9	91	4	AB20163 Protein #
22	32	14.9	91	4	AA667933 Human bon
23	32	14.9	91	4	AAV55549 Human bra
24	32	14.9	91	4	ABG49576 Human liv
25	32	14.9	91	4	AA03485 Peptide #
				5	ABG37468 Human pep

Aam81775 Human hae  
Aam80435 Human hae  
Aaol0522 Human pol  
Abt58386 Human NOV  
Abp42373 Human ova  
Aap80911 Consensus  
Adf69111 Human lun  
Aam23760 Human EST  
Aap70590 Sequence  
Aap70155 Sequence  
ADP55319 Human mhc  
ADJ75476 Marker ge  
ADP12599 Protein e  
ADP12521 Protein e  
Aau32882 Novel hum  
Aa006772 Human pol  
Aas58497 Lung canc  
Adh48788 NOV31 pro  
Ade40250 Human NOV  
ABO57455 Human gen

## ALIGNMENTS

RESULT 1  
AAG64619  
ID AAG64619 standard; protein; 215 AA.  
XX  
AC AAG64619;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human cancer cell specific HLA-F antigen SEQ ID 6.  
XX  
KW HLA-F antigen; cancer cell specific; human.  
XX  
OS Homo sapiens.  
XX  
PN JP2001095584-A.  
XX  
PD 10-APR-2001.  
XX  
PF 30-SEP-1999; 99JP-00279566.  
XX  
PR 30-SEP-1999; 99JP-00279566.  
XX  
PA (EGAW/) EGAWA K.  
PA (MEDI-) MEDINET KK.  
PA (KIMU/) KIMURA K.  
DR WPI; 2001-360493/38.  
DR N-PSDB; AAH45557.  
XX  
PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
XX  
PS Claim 1; Page 11-12; 12pp; Japanese.  
XX  
CC This invention relates to a cancer cell specific HLA-F antigen. The  
CC invention includes DNA encoding the antigen, and a method for the  
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
CC used in a method to diagnose cancer, in which the protein is used to  
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
CC sequence represents the cancer cell-specific HLA-F antigen of the  
CC invention  
XX  
SQ Sequence 215 AA;

Query Match 55.3%; Score 119; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 97 DGKDYISINELRSWTAADTVAQITQRFVEAEYAEFRNYLEGECLLELLRYLENGKET 156

Db 97 DGKDYISLNEDLSRWTAADTAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156  
 QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215  
 Db 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215

RESULT 2

ADP55589  
 ID ADP55589 standard; protein; 215 AA.  
 AC ADP55589;  
 XX  
 DT 12-FEB-2004 (first entry)  
 DE Fragment #2 of human cancer-cell specific HLA-F antigen.  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX  
 OS Homo sapiens.  
 XX JP2003012544-A.  
 PN 15-JAN-2003.  
 PD  
 XX 27-MAR-2002; 2002JP-00089991.  
 PF  
 XX 27-MAR-2001; 2001JP-00090121.  
 PR  
 PA (EGAWA/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU/) KIMURA Y.  
 XX  
 DR WPI; 2003-486263/46.  
 DR N-PSDB; ADP55586.  
 XX  
 PT Agent for preventing and treating cancer, comprising human leukocyte  
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
 XX  
 PS Claim 7; SEQ ID NO 6; 19pp; Japanese.  
 CC The present invention relates to an agent for preventing or treating  
 CC cancer. The agent comprises a portion or a complete sequence of a human  
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
 CC restricted to the major histocompatibility complex (MHC) and specific  
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
 CC is useful for treating or preventing cancer. A cell capable of presenting  
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
 CC for diagnosing cancer. The present sequence represents part of the human  
 CC cancer-cell specific HLA-F antigen.  
 XX  
 SQ Sequence 215 AA;  
 Query Match 55.3%; Score 119; DB 7; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWTAADTAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156  
 Db 97 DGKDYISLNEDLSRWTAADTAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156  
 QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215  
 Db 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215

RESULT 3

AAB43986  
 ID AAB43986 standard; protein; 271 AA.  
 AC AAB43986;  
 XX  
 DT 08-FEB-2001 (first entry)  
 DE Human cancer associated protein sequence SEQ ID NO:1431.  
 DE  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;  
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;  
 KW dermatologic; neuroprotective; thrombolytic; coagulant; neotropic;  
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 OS Homo sapiens.  
 XX WO2000055350-A1.  
 PN 21-SEP-2000.  
 PD  
 XX 08-MAR-2000; 2000WO-US005882.  
 PF  
 XX 12-MAR-1999; 99US-0124270P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Rosen CA, Ruben SM;  
 DR WPI; 2000-587533/55.  
 DR N-PSDB; AAC78195.  
 XX  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.  
 XX  
 PS Claim 11; Page 2115-2116; 2352pp; English.  
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB43986 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnary; immunomodulator;  
 CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; coagulant;  
 CC dermatologic; neuroprotective; thrombolytic; antipsoriatic; antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Pelynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 271 AA;  
 Query Match 55.3%; Score 119; DB 3; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWTAADTAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156  
 Db 146 DGKDYISLNEDLSRWTAADTAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 205

QY 157 LQRADPPKARVVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 215  
 |||||  
 Db 206 LQRADPPKARVVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 264  
 |||||

## RESULT 4

AAG64618  
 ID AAG64618 standard; protein; 274 AA.

AC AAG64618;  
 DT 12-SEP-2001 (first entry)  
 DE Human cancer cell specific HLA-F antigen SEQ ID 5.  
 XX HLA-F antigen; cancer cell specific; human.  
 OS Homo sapiens.

PN JP2001095584-A.  
 PD 10-APR-2001

PF 30-SEP-1999; 99JP-00279566.  
 PR 30-SEP-1999; 99JP-00279566.

PA (EGAW//) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU//) KIMURA Y.

XX WPI; 2001-360493/38.  
 DR N-PSDB; AAF45556.

XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.

PT Claim 2; Page 10-11; 12pp; Japanese.

PS This invention relates to a cancer cell specific HLA-F antigen. The  
 CC invention includes DNA encoding the antigen, and a method for the  
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
 CC used in a method to diagnose cancer, in which the protein is used to  
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
 CC sequence represents the cancer cell-specific HLA-F antigen of the  
 CC invention

XX SQ Sequence 274 AA;

Query Match 55.3%; Score 119; DB 4; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISNEDLSRWTAADTVAQITQRYEAEYAEFFRYLGECLLRRYLENGKET 156  
 |||||  
 Db 119 DGKDYISNEDLSRWTAADTVAQITQRYEAEYAEFFRYLGECLLRRYLENGKET 178  
 |||||

QY 157 LQRADPPKARVVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 215  
 |||||  
 Db 179 LQRADPPKARVVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 237  
 |||||

## RESULT 5

ADP55588  
 ID ADP55588 standard; protein; 274 AA.

AC ADP55588;  
 DT 12-FEB-2004 (first entry)  
 DE Fragment #1 of human cancer-cell specific HLA-F antigen.  
 XX Cancer; human leukocyte antigen-F; HLA-F;

PN JP2001095584-A.  
 PD 10-APR-2001.

PF 30-SEP-1999; 99JP-00279566.

KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.

XX Homo sapiens.

PN JP2003012544-A.

XX 15-JAN-2003.

PF 27-MAR-2002; 2002JP-00088991.

PR 27-MAR-2001; 2001JP-00090121.

XX (EGAW//) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU//) KIMURA Y.

XX WPI; 2003-486263/46.  
 DR N-PSDB; ADF55585.

XX Agent for preventing and treating cancer, comprising human leukocyte  
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.

PS Claim 7; SEQ ID NO 5; 19pp; Japanese.

XX The present invention relates to an agent for preventing or treating  
 CC cancer. The agent comprises a portion or a complete sequence of a human  
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
 CC unrestricted to the major histocompatibility complex (MHC) and specific  
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
 CC is useful for treating or preventing cancer. A cell capable of presenting  
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
 CC for diagnosing cancer. The present sequence represents part of the human  
 CC cancer-cell specific HLA-F antigen.

XX SQ Sequence 274 AA;

Query Match 55.3%; Score 119; DB 7; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISNEDLSRWTAADTVAQITQRYEAEYAEFFRYLGECLLRRYLENGKET 156  
 |||||  
 Db 119 DGKDYISNEDLSRWTAADTVAQITQRYEAEYAEFFRYLGECLLRRYLENGKET 178  
 |||||

QY 157 LQRADPPKARVVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 215  
 |||||  
 Db 179 LQRADPPKARVVAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 237  
 |||||

## RESULT 6

AAG64617  
 ID AAG64617 standard; protein; 362 AA.

AC AAG64617;

XX 12-SEP-2001 (first entry)

DE Human cancer cell specific HLA-F antigen SEQ ID 4.

XX HLA-F antigen; cancer cell specific; human.

XX Homo sapiens.

PN JP2001095584-A.

PD 10-APR-2001.

PF 30-SEP-1999; 99JP-00279566.

XX

PR 30-SEP-1999; 99JP-00279566.  
 XX (EGAW//) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU//) KIMURA K.  
 XX  
 DR WPI; 2001-360493/38.  
 DR N-PSDB; AAH45555.  
 XX  
 PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
 XX Disclosure; Page 9-10; 12pp; Japanese.  
 CC This invention relates to a cancer cell specific HLA-F antigen. The  
 CC invention includes DNA encoding the antigen, and a method for the  
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
 CC used in a method to diagnose cancer, in which the protein is used to  
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
 CC sequence represents the cancer cell-specific HLA-F antigen of the  
 CC invention  
 XX  
 XX Sequence 362 AA;  
 Query Match 55.3%; Score 119; DB 4; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 97 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 156  
 DB 140 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 199  
 QY 157 LQRADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEIRPAG 215  
 DB 200 LQRADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEIRPAG 259  
 RESULT 7  
 ABB50296  
 ID ABB50296 standard; protein; 362 AA.  
 XX  
 AC ABB50296;  
 XX  
 DT 08-FEB-2002 (first entry)  
 XX  
 DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.  
 XX  
 KW Ovarian tumour marker gene; human; overexpression; upregulation;  
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;  
 KW identification; serous cystadenoma; borderline serous tumour;  
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;  
 KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;  
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;  
 KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;  
 KW immune response pathway; cell proliferation regulation; protein folding;  
 KW membrane localised; secreted; therapeutic target; cytostatic;  
 KW gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175177-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 03-APR-2001; 2001WO-US010947.  
 XX  
 PR 03-APR-2000; 2000US-0194336P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;  
 DR WPI; 2001-626450/72.  
 DR N-PSDB; ABA83122.

XX Detecting and identifying ovarian tumor, identifying increased risk for  
 PT developing ovarian cancer, and determining effectiveness of ovarian  
 PT cancer treatment, by measuring expression level of ovarian tumor marker  
 PT gene.  
 XX  
 PS Claim 23; Page 126-127; 140pp; English.  
 XX  
 CC The invention relates to methods for diagnosing and prognosing ovarian  
 CC tumors in an individual via the detection and measurement of the  
 CC expression of ovarian tumor marker genes (ABA83081-ABA83122, ABA83180,  
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,  
 CC ABA83181 and ABA83183). The methods of the invention are useful for  
 CC detecting an ovarian tumor in a patient, for identifying an individual  
 CC at increased risk for developing ovarian cancer, in prognostic tests for  
 CC assessing the relative severity of ovarian cancer, in tests for  
 CC monitoring a patient in remission from ovarian cancer and in tests for  
 CC monitoring disease status in a patient being treated for ovarian cancer.  
 CC The methods can additionally be used to identify a particular tumor as  
 CC being an ovarian tumor (i.e., an epithelial ovarian tumor selected from  
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,  
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous  
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,  
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner  
 CC tumour. The ovarian tumor marker genes of the invention were identified  
 CC using SAGE (serial analysis of gene expression) and were found to be  
 CC overexpressed in a broad variety of ovarian epithelial tumour cells  
 CC relative to normal ovarian epithelial cells. The marker genes are  
 CC implicated in immune response pathways, in the regulation of cell  
 CC proliferation and in protein folding, and many of these are membrane-  
 CC localised or secreted. In addition to their use as diagnostic and  
 CC prognostic markers, the ovarian tumour marker genes or their encoded  
 CC proteins may be used as therapeutic targets for the treatment and  
 CC prevention of ovarian cancer. Sequences ABB50257-ABB50399 represent  
 CC proteins encoded by ovarian tumour marker genes of the invention  
 XX  
 XX Sequence 362 AA;  
 Query Match 55.3%; Score 119; DB 4; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 97 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 156  
 DB 140 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 199  
 QY 157 LQRADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEIRPAG 215  
 DB 200 LQRADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEIRPAG 258  
 RESULT 8  
 ADF55587  
 ID ADF55587 standard; protein; 362 AA.  
 XX  
 AC ADF55587;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human cancer-cell specific HLA-F antigen.  
 XX  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2003012544-A.  
 XX  
 PD 15-JAN-2003.  
 XX  
 PF 27-MAR-2002; 2002JP-00088991.  
 XX

PR 27-MAR-2001; 2001JP-00090121.  
 XX (EGAWA/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KING/) KIMURA Y.  
 XX WPI; 2003-486263/46.  
 DR N-PSDB; ADF55384.  
 XX  
 XX Agent for preventing and treating cancer, comprising human leukocyte  
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
 XX  
 XX Claim 5; SEQ ID NO 4; 19pp; Japanese.  
 XX  
 CC The present invention relates to an agent for preventing or treating  
 CC cancer. The agent comprises a portion or a complete sequence of a human  
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
 CC unrestricted to the major histocompatibility complex (MHC) and specific  
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
 CC is useful for treating or preventing cancer. A cell capable of presenting  
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
 CC for diagnosing cancer. The present sequence represents human cancer-cell  
 CC specific HLA-F antigen.  
 XX  
 XX Sequence 362 AA;  
 SQ  
 Query Match 55.3%; Score 119; DB 7; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 97 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 156  
 DB 140 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 199  
 QY 157 LQRADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 215  
 DB 200 LQRADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 259  
 RESULT 9  
 ADJ75372  
 ID ADJ75372 standard; protein; 362 AA.  
 XX  
 AC ADJ75372;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Marker gene related amino acid sequence SEQ ID NO:624.  
 XX  
 KW bronchial asthma; chronic obstructive pulmonary disease;  
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
 KW gene therapy; marker.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1394274-A2.  
 XX  
 PD 03-MAR-2004.  
 XX  
 PF 04-AUG-2003; 2003EP-00254857.  
 XX  
 PR 06-AUG-2002; 2002JP-00229312.  
 PR 20-MAR-2003; 2003JP-00077212.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;  
 XX WPI; 2004-193155/19.  
 DR

PT Testing for bronchial asthma or chronic obstructive pulmonary disease by  
 PT comparing the expression level of a marker gene in a biological sample  
 PT from a subject with the expression level of the gene in a sample from a  
 PT healthy subject.  
 XX  
 XX Example 11; SEQ ID NO 624; 241pp; English.  
 XX  
 CC The present invention describes a method of testing for bronchial asthma  
 CC or chronic obstructive pulmonary disease. The method comprises  
 CC determining the expression level of a marker gene in a biological sample  
 CC from a subject, comparing the expression level determined with the  
 CC expression level of the marker gene in a biological sample from a healthy  
 CC subject, and judging whether the subject has bronchial asthma or chronic  
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
 CC genes (S1) whose expression levels increase when respiratory epithelial  
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
 CC whose expression levels decrease when respiratory epithelial cells are  
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
 CC (2) a kit for screening for a candidate compound for a therapeutic agent  
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
 CC an animal model for bronchial asthma or chronic obstructive pulmonary  
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
 CC method for producing an animal model for bronchial asthma or chronic  
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
 CC the marker gene or an antisense nucleic acid corresponding to a portion of  
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
 CC expression of the gene through an RNAi effect or an antibody recognising  
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
 CC probe has been immobilised to assay a marker gene. (I) has respiratory  
 CC and antiasthmatic activities, and can be used in gene therapy. The method  
 CC is useful for testing for or screening for a therapeutic agent for  
 CC bronchial asthma or chronic obstructive pulmonary disease. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX  
 XX Sequence 362 AA;  
 SQ  
 Query Match 55.3%; Score 119; DB 8; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 97 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 156  
 DB 140 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 199  
 QY 157 LQRADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 215  
 DB 200 LQRADPPKHAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 258  
 RESULT 10  
 ADP12500  
 ID ADP12500 standard; protein; 362 AA.  
 XX  
 AC ADP12500;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Protein encoded by mRNA of the invention #110.  
 XX  
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;  
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004042346-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 24-APR-2003; 2003WO-US012946.  
 XX

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PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2509; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
SQ Sequence 362 AA;
Query Match 55.3%; Score 119; DB 8; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.1e-107;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFTYLEGSCLELLRRYLENGKET 156
DB 140 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFTYLEGSCLELLRRYLENGKET 199
QY 157 LQADPPKAAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQDTDELVETRPAG 215
DB 200 LQADPPKAAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQDTDELVETRPAG 258
RESULT 11
ADJ70081
XX ADJ70081 standard; protein; 442 AA.
XX
AC ADJ70081;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID1887.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.

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PR 17-JUN-2002; 2002US-038987P.
PR 20-SEP-2002; 2002US-0412418P.
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Faby ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX
CC Identifying a mitochondrial target for drug screening assays and for
CC treating diseases associated with altered mitochondrial function,
CC comprises detecting a modified polypeptide in a sample and correlating
CC with the disease.
XX
PS Claim 1; SEQ ID NO 1887; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 442 AA;
Query Match 55.3%; Score 119; DB 7; Length 442;
Best Local Similarity 100.0%; Pred. No. 6.1e-107;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFTYLEGSCLELLRRYLENGKET 156
DB 140 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFTYLEGSCLELLRRYLENGKET 199
QY 157 LQADPPKAAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQDTDELVETRPAG 215
DB 200 LQADPPKAAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQDTDELVETRPAG 258
RESULT 12
ABG26726
ID ABG26726 standard; protein; 677 AA.
XX
AC ABG26726;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26717.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.

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PA (HYSE-) HYSEQ INC.  
 XX Drmanac RT, Liu C, Tang YT;  
 PI WPI; 2001-639362/73.  
 DR N-PSDB; AAS90913.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX Claim 20; SEQ ID NO 57085; 103pp; English.  
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ASG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: the sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 677 AA;  
 SQ Query Match 55.3%; Score 119; DB 4; Length 677;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-107;  
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 97 DGDVLSNEDLSRWTAADTAQITQRYEAEVYAEAEFRVLEGECLLRRVLENGKET 156  
 DB 449 DGDVLSNEDLSRWTAADTAQITQRYEAEVYAEAEFRVLEGECLLRRVLENGKET 508  
 QY 157 LQADPPKAAVHAHPSDHEATLRCWALGFYPAEITLTWQDGEQDTLVEVTRPAG 215  
 DB 509 LQADPPKAAVHAHPSDHEATLRCWALGFYPAEITLTWQDGEQDTLVEVTRPAG 567  
 RESULT 13  
 AAG00209  
 ID AAG00209 standard; protein; 120 AA.  
 XX AAG00209;  
 AC AAG00209;  
 DT 06-OCT-2000 (first entry)  
 XX Human secreted protein, SEQ ID NO: 4290.  
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 XX gene therapy; chromosome mapping.  
 KW Homo sapiens.  
 XX EP1033401-A2.  
 XX 06-SEP-2000.  
 XX 21-FEB-2000; 2000EP-00200610.  
 XX 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 PI WPI; 2000-500381/45.  
 DR N-PSDB; AAC00215.  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.  
 XX The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 CC sequences derived from the 5' ends of mRNAs and even in those cases where  
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 CC are also used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. They are used to obtain upstream regulatory sequences  
 CC and to design expression and secretion vectors  
 XX Sequence 120 AA;  
 SQ Query Match 35.8%; Score 77; DB 3; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-66;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IAVEYVDDTQFLRPSDAAIPRMEPRPWPVEQSGPQYWEWTTGYAKANAQTDRAVALNLL 60  
 DB 44 IAVEYVDDTQFLRPSDAAIPRMEPRPWPVEQSGPQYWEWTTGYAKANAQTDRAVALNLL 103  
 QY 61 RRYNQSEAGSHTLQGMN 77  
 DB 104 RRYNQSEAGSHTLQGMN 120  
 RESULT 14  
 ABO57084  
 ID ABO57084 standard; protein; 96 AA.  
 XX ABO57084;  
 AC ABO57084;  
 XX 29-JUL-2004 (first entry)  
 DT Human genome derived single exon protein #3318.  
 DE Human; gene expression; single exon probe; microarray;  
 XX alternative splicing event; genomic alteration.  
 KW Homo sapiens.  
 XX OS  
 XX US2003194704-A1.  
 XX 16-OCT-2003.  
 XX 03-APR-2002; 2002US-00029386.  
 XX 03-APR-2002; 2002US-00029386.  
 XX (PENN/) PENN S G.  
 XX (RANK/) RANK D R.  
 XX (HANZ/) HANZEL D K.  
 XX Penn SG, Rank DR, Hanzel DK;  
 XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human  
PT gene expression analysis, for identifying or characterizing alternative  
PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.

PS Claim 45; SEQ ID NO 30718; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene  
CC expression, comprising any of the 27,400 fully defined nucleotide  
CC sequences in the specification, or their complements or fragments, and  
CC encoding at least 8 amino acids of any of the 6988 amino acid sequences  
CC fully defined in the specification. The probe is a single exon probe that  
CC hybridises under high stringency conditions to a nucleic acid molecule  
CC expressed in human cells or tissues. Also included are a spatially-  
CC addressable set of single exon nucleic acid probes for measuring human  
CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC methods of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above. The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterising  
CC alternative splicing events, in detecting and characterising gross  
CC alterations in the genomic locus that includes their exon. In assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence is a human  
CC single exon probe protein of the invention. Note: the sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC segdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 96 AA;

Query Match 25.6%; Score 55; DB 8; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.8e-45;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 DPPKHAHVHPISDHEATLRCWALGFPYPAITITLWQDGEETQDTLVEVTPAG 215

Db 2 DPPKHAHVHPISDHEATLRCWALGFPYPAITITLWQDGEETQDTLVEVTPAG 56

RESULT 15

ABP42931

ID ABP42931 standard; protein; 186 AA.

XX ABP42931;

XX 22-AUG-2002 (first entry)

DE Human ovarian antigen HPDRT37, SEQ ID NO:4063.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW Gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ56008.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
PT cancer), immune disorders, cardiovascular disorders and neurological  
PT diseases.

XX Claim 11; SEQ ID NO 4063; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents a human ovarian antigen of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 186 AA;

Query Match 24.2%; Score 52; DB 5; Length 186;

Best Local Similarity 100.0%; Pred. No. 3.9e-42;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YAKANAQTDVRLNLLRRYQSEAGSHTLQMGNCMDGPDGRLRGYHOHA 95

Db 1 YAKANAQTDVRLNLLRRYQSEAGSHTLQMGNCMDGPDGRLRGYHOHA 52

Search completed: December 15, 2004, 18:20:04

Job time : 97.8487 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:30 ; Search time 142.323 seconds  
(without alignments)  
1107.709 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYFSTAVSRPGRGP.....QRYTCHVQHGLPQLRLW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	274	100.0	324	2 Q861E9	Q861E9 homo sapien
2	274	100.0	324	2 Q861F0	Q861F0 homo sapien
3	274	100.0	346	2 Q8WLP5	Q8WLP5 homo sapien
4	274	100.0	346	2 Q6DU28	Q6DU28 homo sapien
5	274	100.0	346	2 AAH62991	AAH62991 homo sapi
6	274	100.0	362	1 HLA-F HUMAN	P30511 homo sapien
7	274	100.0	362	2 BAC54915	BAC54915 homo sapi
8	274	100.0	460	2 Q8SHC0	Q8SHC0 homo sapien
9	250	91.2	346	2 Q8MGQ1	Q8MGQ1 homo sapien
10	224	81.8	346	2 Q6DU20	Q6DU20 homo sapien
11	208	75.9	346	2 Q95IT2	Q95IT2 pan troglod
12	208	75.9	362	2 Q7YR27	Q7YR27 pan troglod
13	182	66.4	254	2 Q860R0	Q860R0 homo sapien
14	126	46.0	346	1 IC28 PANTR	P16215 pan troglod
15	108	39.4	349	2 Q8ZUN0	Q8ZUN0 homo sapien
16	108	39.4	349	2 BAC86108	BAC86108 homo sapi
17	87	31.8	91	2 Q9TPX7	Q9TPX7 gorilla gor
18	73	26.6	316	2 Q93958	Q93958 homo sapien
19	62	22.6	314	2 Q860F6	Q860F6 macaca neme
20	61	22.3	353	2 Q9MXS6	Q9MXS6 macaca mula
21	61	22.3	353	2 Q9MXS7	Q9MXS7 macaca mula
22	61	22.3	354	2 Q70UE5	Q70UE5 macaca mula
23	61	22.3	354	2 Q70UE6	Q70UE6 macaca mula
24	61	22.3	354	2 Q70UE7	Q70UE7 macaca mula
25	61	22.3	354	2 CAD65766	CAD65766 macaca mu
26	61	22.3	354	2 CAD65765	CAD65765 macaca mu
27	61	22.3	354	2 CAD65767	CAD65767 macaca mu
28	61	22.3	365	2 Q9MXS5	Q9MXS5 macaca mula
29	59	21.5	59	2 Q78094	Q78094 homo sapien
30	59	21.5	348	1 HLA-F MACMU	P33617 macaca mula
31	58	21.2	354	2 Q70SIO	Q70SIO macaca mula

32	58	21.2	354	2 CAD83073	CAD83073 macaca mu
33	58	21.2	365	2 Q617A3	Q617A3 macaca fasc
34	55	20.1	365	2 Q617A9	Q617A9 macaca fasc
35	53	19.3	354	2 Q70SH4	Q70SH4 macaca mula
36	53	19.3	354	2 CAD83079	CAD83079 macaca mu
37	53	19.3	355	2 Q767W6	Q767W6 aotus tri
38	53	19.3	355	2 BAD18842	BAD18842 aotus tri
39	53	19.3	365	2 Q61796	Q61796 macaca fasc
40	50	18.2	351	2 Q70PL7	Q70PL7 macaca mula
41	50	18.2	351	2 Q70FMO	Q70FMO macaca mula
42	50	18.2	351	2 CAD89636	CAD89636 macaca mu
43	50	18.2	351	2 CAD89639	CAD89639 macaca mu
44	45	16.4	330	2 Q30713	Q30713 macaca mula
45	45	16.4	338	2 Q95510	Q95510 leopardus p

## ALIGNMENTS

### RESULT 1

Q861E9	PRELIMINARY;	PRT;	324 AA.
AC	Q861E9		
DT	01-JUN-2003 (Tremblrel. 24, Created)		
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	MHC class I antigen (Fragment)		
GN	Name=HLA-F;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Liu Y., Xu L., Zeng Y., He X.;		
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY221102; AAC34407.1; -		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG-cl.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR001039; MHC_I.		
DR	Pfam; PF07654; CL-set; 1.		
DR	Pfam; PF00129; MHC_I; 1.		
DR	PRINTS; PR01638; MHCCLASSI.		
DR	ProDom; PD000050; MHC_I; 1.		
DR	PROSITE; PS00835; IG LIKE; 1.		
DR	PROSITE; PS00290; IG_MHC; 1.		
FT	NON_TER	324	
SQ	SEQUENCE	324 AA;	E3E028177D2716F4 CRC64;

Query Match	100.0%;	Score 274;	DB 2;	Length 324;
Best Local Similarity	100.0%;	Pred. No. 3.3e-280;		
Matches 274;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GSHSLRYFSTAVSRPGRGPRIAYEVVDVDTQFLRDSDAIIPMEPRPFWVEQGPQYW	60
Db	18	GSHSLRYFSTAVSRPGRGPRIAYEVVDVDTQFLRDSDAIIPMEPRPFWVEQGPQYW	77
QY	61	EWTGYAKANAQTDVRLNLLRRYNQSEAGSHTLQMGNCMDGPDGRLRGYHQHAYDG	120
Db	78	EWTGYAKANAQTDVRLNLLRRYNQSEAGSHTLQMGNCMDGPDGRLRGYHQHAYDG	137
QY	121	KDYISLNEEDLSWTAADTVAQITQRFYAEYAEAEERTYLEGCELLRRYLENGKETIQ	180
Db	138	KDYISLNEEDLSWTAADTVAQITQRFYAEYAEAEERTYLEGCELLRRYLENGKETIQ	197
QY	181	RADPFAKVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQTOQTELVEITRPAGDGT	240
Db	198	RADPFAKVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQTOQTELVEITRPAGDGT	257

QY 241 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLLRW 274  
 DB |||||||  
 258 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLLRW 291  
 |||||||

## RESULT 2

Q861F0 PRELIMINARY; PRT; 324 AA.  
 AC Q861F0;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Nonclassical MHC class I antigen (fragment).  
 GN Name=HLA-F;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA He X., Xu L., Liu Y., Zeng Y.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY216682; AAC37689.1; -;  
 DR HSSP; Q29361; IHS4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SMO0407; IGC1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_VHC; 1.  
 FT NON\_TER 1 324  
 FT NON\_TER 324 324  
 SQ SEQUENCE 324 AA; 36518 MW; E3E028177D271654 CRC64;

Query Match 100.0%; Score 274; DB 2; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 3,3e-280;  
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRFSTAVSPGEGEPRYIAVYVDDTQFLRFDSDAAIPRPEPFWVEQGPQYW 60  
 DB |||||||  
 18 GSHSLRFSTAVSPGEGEPRYIAVYVDDTQFLRFDSDAAIPRPEPFWVEQGPQYW 77  
 |||||||  
 QY 61 EWTGKAKANAQTDVRLNRLRRYVQSEAGSHLQGMNGCDWGPDRLLRGYHQHAYDG 120  
 DB |||||||  
 78 EWTGKAKANAQTDVRLNRLRRYVQSEAGSHLQGMNGCDWGPDRLLRGYHQHAYDG 137  
 |||||||  
 QY 121 KQYISINEDRSWTAATVAQITQRYEAEYAEPRTYLEGCELLRRYLENGKETLQ 180  
 DB |||||||  
 138 KQYISINEDRSWTAATVAQITQRYEAEYAEPRTYLEGCELLRRYLENGKETLQ 197  
 |||||||  
 QY 181 RADPPKAVAHPTSDHEATLRCWALGFYPAEITLTWQRDGEQQTDLVETRPAGDGT 240  
 DB |||||||  
 198 RADPPKAVAHPTSDHEATLRCWALGFYPAEITLTWQRDGEQQTDLVETRPAGDGT 257  
 |||||||  
 QY 241 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLLRW 274  
 DB |||||||  
 258 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLLRW 291  
 |||||||

## RESULT 3

Q8WLP5 PRELIMINARY; PRT; 346 AA.  
 AC Q8WLP5;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE MHC class Ib antigen (HLA-F protein).  
 GN Name=HLA-F;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA He X., Xu L., Liu Y., Zeng Y.;  
 RL Identification of a novel HLA-F allele - HLA-F\*010102.;  
 RN Tissue Antigens 63:181-183(2004).  
 RP SEQUENCE FROM N.A.  
 RA He X., Xu L., Liu Y., Zeng Y.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting V., Young A.C., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Pvo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AS523285; RAM74980.1; -;  
 DR EMBL; AF523288; RAM74982.1; -;  
 DR EMBL; AF523288; RAM74983.1; -;  
 DR EMBL; AF523289; RAM74984.1; -;  
 DR EMBL; AF523290; RAM74985.1; -;  
 DR EMBL; AF523293; RAM74988.1; -;  
 DR EMBL; AF523294; RAM74989.1; -;  
 DR EMBL; AF523295; RAM74990.1; -;  
 DR EMBL; AF523296; RAM74991.1; -;  
 DR EMBL; AF523297; RAM74992.1; -;  
 DR EMBL; AY253270; AAO86773.1; -;  
 DR EMBL; AY253270; AAO86774.1; -;  
 DR EMBL; BC062991; AAH62991.1; -;  
 DR EMBL; AY645742; RAT73225.1; -;  
 DR EMBL; AY645743; RAT73226.1; -;  
 DR EMBL; AY645744; RAT73227.1; -;  
 DR EMBL; AY645745; RAT73228.1; -;  
 DR EMBL; AY645746; RAT73229.1; -;  
 DR EMBL; AY645749; RAT73232.1; -;  
 DR EMBL; AY645750; RAT73233.1; -;

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DR EMBL; AY645751; AAT73234.1; -
DR EMBL; AY645752; AAT73235.1; -
DR EMBL; AY645753; AAT73236.1; -
DR EMBL; AY645756; AAT73239.1; -
DR EMBL; AY645757; AAT73240.1; -
DR EMBL; AY645758; AAT73241.1; -
DR EMBL; AY645759; AAT73242.1; -
DR EMBL; AF523286; AAM74981.1; -
DR HSSP; Q29961; 1HSA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC I; 1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Transmembrane.
SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 100.0%; Score 274; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.5e-280;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81
QY 61 EWTTCYAKANAQTDVALNRLRRYNOSEAGSHTLQMGNGCDMPDGLRLRGYHQYADG 120
DB 82 EWTTCYAKANAQTDVALNRLRRYNOSEAGSHTLQMGNGCDMPDGLRLRGYHQYADG 141
QY 121 KDYISLNEDLSRWTAAADTVAQITQRFYAEAYEAEFRTYLEGCELELLRYLNGKETLQ 180
DB 142 KDYISLNEDLSRWTAAADTVAQITQRFYAEAYEAEFRTYLEGCELELLRYLNGKETLQ 201
QY 181 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVELTRPAGDGT 240
DB 202 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVELTRPAGDGT 261
QY 241 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 274
DB 262 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 295

RESULT 4
Q6DU28 PRELIMINARY; PRT; 346 AA.
AC Q6DU28;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY645747; AAT73230.1; -
DR EMBL; AY645748; AAT73231.1; -
SQ SEQUENCE 346 AA; 39079 MW; 8C370BFB40B15818 CRC64;

Query Match 100.0%; Score 274; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.5e-280;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GSHSLRYFSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81
QY 61 EWTTCYAKANAQTDVALNRLRRYNOSEAGSHTLQMGNGCDMPDGLRLRGYHQYADG 120
DB 82 EWTTCYAKANAQTDVALNRLRRYNOSEAGSHTLQMGNGCDMPDGLRLRGYHQYADG 141
QY 121 KDYISLNEDLSRWTAAADTVAQITQRFYAEAYEAEFRTYLEGCELELLRYLNGKETLQ 180
DB 142 KDYISLNEDLSRWTAAADTVAQITQRFYAEAYEAEFRTYLEGCELELLRYLNGKETLQ 201
QY 181 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVELTRPAGDGT 240
DB 202 RADPPKAVHAPHSIDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVELTRPAGDGT 261
QY 241 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 274
DB 262 FOKWAAVVVPSGEGEORYTCHVQHEGLPQPLILRW 295

RESULT 5
AAH62991 PRELIMINARY; PRT; 346 AA.
AC AAH62991;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE HLA-F protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062991; AAH62991.1; -
SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 100.0%; Score 274; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.5e-280;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GSHSLRYFSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81

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QY 61 EMTTCYAKAQAQTDVVALNRLRYNSOAGSHLTQMGNGCMGPDGRLRGRHYGHAYDG 120  
 DB 82 EMTTCYAKAQAQTDVVALNRLRYNSOAGSHLTQMGNGCMGPDGRLRGRHYGHAYDG 141  
 QY 121 KYDISLNEDLRSWTAADTAQITQRFVYAEABEYFETYLEGECLELLRRYLENGKETLQ 180  
 DB 142 KYDISLNEDLRSWTAADTAQITQRFVYAEABEYFETYLEGECLELLRRYLENGKETLQ 201  
 QY 191 RADPKKAVAHHPISDHEATLRWALGFYDAEITLTWQDGEQOTDELVETRPAGDGT 240  
 DB 202 RADPKKAVAHHPISDHEATLRWALGFYDAEITLTWQDGEQOTDELVETRPAGDGT 261  
 QY 241 FQKWAUVVPSGEBQRYTCHVQHEGLPQPLILRW 274  
 DB 262 FQKWAUVVPSGEBQRYTCHVQHEGLPQPLILRW 295

## RESULT 6

HLAF HUMAN STANDARD; PRT; 362 AA.  
 AC P30511; Q3TP68;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (leukocyte antigen F) (CDAL2).  
 GN Name=HLA-F; Synonyms=HLAF, HLA-5.4;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90111605; PubMed=1689605;  
 RA Geraghty D.E., Wei X., Ori H.T., Koller B.H.;  
 RT "Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element.";  
 RT J. Exp. Med. 171:1-18(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91197889; PubMed=1707659;  
 RA Lury D., Epstein H., Holmes N.;  
 RT "The human class I MHC gene HLA-F is expressed in lymphocytes.";  
 RT Int. Immunol. 2:531-537(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20189617; PubMed=10727083;  
 RA Hampe A., Coriton O., Andrieux N., Carn G., Lepourcellet M.,  
 RA Mortier S., Drenon S., Gaius M.T., Hitt C., Soriano N., Galibert F.;  
 RT "A 356-Kb sequence of the subtelomeric part of the MHC class I region.";  
 RT DNA Seq. 10:263-299(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX SHINA S., Tamiya G., Oka A., Inoko H.;  
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A., AND VARIANT PRO-272.  
 RX MEDLINE=22933763; PubMed=14574404; DOI=10.1038/nature02055;  
 RA Mungall A.J., Palmer M.C., Sims S.K., Edwards C.A., Ashurst J.L.,  
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,  
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,  
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,  
 RA Babage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,  
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,  
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,  
 RA Burford D.C., Burrill W., Burton J., Carter C., Carter N.P.,  
 RA Chapman J.C., Clark Y., Clark G., Clee C.M., Clegg S., Cobley V.,  
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,  
 RA Cully K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,

RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,  
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,  
 RA Gilby L.M., Gillson C.J., Glithero R.J., Graham D.V., Grant M.,  
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,  
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote E.,  
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,  
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,  
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,  
 RA Lawlor S., Leongamornleet D.A., Leversha M., Lloyd C.R., Lloyd D.M.,  
 RA Loveland J.E., Lovell J., Martin S., Mashreshi-Mohammadi M.,  
 RA Maslen G.L., Matthews L., McGann O.T., McIsken S.J., McIay K.,  
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,  
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,  
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,  
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,  
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Straggon L.,  
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,  
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,  
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Wray P.W.,  
 RA Whittaker H., Wild A., Willey D.J., Wilmer F.E., Wood J.M., Wyatt J.C.,  
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,  
 RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;  
 RT "The DNA sequence and analysis of human chromosome 6.";  
 RL Nature 425:805-811(2003).  
 CC -I- FUNCTION: Involved in the presentation of foreign antigens to the immune system.  
 CC -I- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).  
 CC  
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 CC  
 DR EMBL; X17093; CAA34947.1; -;  
 DR EMBL; AF055066; AAC24827.1; -;  
 DR EMBL; AF000521; BAB63337.1; -;  
 DR EMBL; AL022723; CAB46623.1; -;  
 DR PIR; A60384; A60384.  
 DR HGSP; Q29961; LHSA.  
 DR Genew; HGNC:4963; HLA-F.  
 DR MIM; 143110; -;  
 DR GO; GO:0030106; F:MHC class I receptor activity; TAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR InterPro; IPR010579; MHC\_I\_C.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR Pfam; PF06623; MHC\_I\_C; 1.  
 DR PRINTS; PR01639; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IgC1; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR GlycoProtex; MHC\_I\_Polymorphism; Signal; Transmembrane.  
 KW SIGNAL; 1 21  
 FT CHAIN; 22 362  
 FT  
 FT HLA class I histocompatibility antigen, alpha chain F.  
 FT DOMAIN; 22 111  
 FT DOMAIN; 112 203  
 FT DOMAIN; 204 295  
 FT DOMAIN; 296 305  
 FT DOMAIN; 306 329  
 FT TRANSMEM; 330 362  
 FT DOMAIN; 122 185  
 FT DISULFID; 224 280  
 FT CARBOHYD; 107 107  
 FT VARIANT; 272  
 S -> P (in dbSNP:1736924).

FT SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64; /FTID=VAR\_018327.

Query Match 100.0%; Score 274; DB 1; Length 362;  
Best Local Similarity 100.0%; Pred. No. 3.7e-280;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAI PRMEPRFPWVEQGPQYW 60  
DB 22 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAI PRMEPRFPWVEQGPQYW 81

QY 61 EMTTGAKANAQTDRAVALNLLRRYNQSEAGSHLTQGMNGCDMPDGLLRGVHGHAYDG 120  
DB 82 EMTTGAKANAQTDRAVALNLLRRYNQSEAGSHLTQGMNGCDMPDGLLRGVHGHAYDG 141

QY 121 KYIISINELDRSWTAADVAQITQRFYAEYAEFFRYLGECELELLRYLNGKETLQ 180  
DB 142 KYIISINELDRSWTAADVAQITQRFYAEYAEFFRYLGECELELLRYLNGKETLQ 201

QY 181 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 240  
DB 202 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 261

QY 241 FOKWAAVVPSEGEORYTCHVQHEGLPOPLILRW 274  
DB 262 FOKWAAVVPSEGEORYTCHVQHEGLPOPLILRW 295

RESULT 7  
BAC54915 PRELIMINARY; PRT; 362 AA.

AC BAC54915  
DT 02-MAR-2004 (TRENBLrel. 27, Created)  
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)  
DE Major histocompatibility complex, class I, F.  
GN HLA-F.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;  
RT "Genome diversity in HLA: A new strategy for detection of genetic  
RT polymorphisms in expressed genes within the HLA class III and class I  
RT regions";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB086082; BAC54915.1; --  
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 100.0%; Score 274; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 3.7e-280;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAI PRMEPRFPWVEQGPQYW 60  
DB 22 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAI PRMEPRFPWVEQGPQYW 81

QY 61 EMTTGAKANAQTDRAVALNLLRRYNQSEAGSHLTQGMNGCDMPDGLLRGVHGHAYDG 120  
DB 82 EMTTGAKANAQTDRAVALNLLRRYNQSEAGSHLTQGMNGCDMPDGLLRGVHGHAYDG 141

QY 121 KYIISINELDRSWTAADVAQITQRFYAEYAEFFRYLGECELELLRYLNGKETLQ 180  
DB 142 KYIISINELDRSWTAADVAQITQRFYAEYAEFFRYLGECELELLRYLNGKETLQ 201

QY 181 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 240  
DB 202 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 261

QY 241 FOKWAAVVPSEGEORYTCHVQHEGLPOPLILRW 274  
DB 262 FOKWAAVVPSEGEORYTCHVQHEGLPOPLILRW 295

DB 262 FOKWAAVVPSEGEORYTCHVQHEGLPOPLILRW 295

RESULT 8  
Q95HCO PRELIMINARY; PRT; 460 AA.

AC Q95HCO  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE HLA-F protein (Fragment).  
GN Name=HLA-F;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.

RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009260; AAH09260.2; --  
DR HSSP; Q29961; IHSB.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR001039; MHC I.  
DR Pfam; PF07654; CI-set; 1.  
DR Pfam; PF00129; MHC; 1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR ProDom; PD000050; MHC\_I; 1.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER  
SQ SEQUENCE 460 AA; 52263 MW; CIA0B6891978D93E CRC64;

Query Match 100.0%; Score 274; DB 2; Length 460;  
Best Local Similarity 100.0%; Pred. No. 4.6e-280;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAI PRMEPRFPWVEQGPQYW 60  
DB 40 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAI PRMEPRFPWVEQGPQYW 99

QY 61 EMTTGAKANAQTDRAVALNLLRRYNQSEAGSHLTQGMNGCDMPDGLLRGVHGHAYDG 120

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Db 100 EWTTGYAKANAQTRVALNRLLRRYNQSEAGSHTLQNMNGCDMGPDRLLRCYHGHAYDG 159
Qy 121 KDYISLNEDLSRWTAADTVAAITQRFYEAEYAEAEFRTYLEGECLLELLRRYLENGKETLQ 180
Db 160 KDYISLNEDLSRWTAADTVAAITQRFYEAEYAEAEFRTYLEGECLLELLRRYLENGKETLQ 219
Qy 181 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Db 220 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 279
Qy 241 FQKWAADVVP 250
Db 262 FQKWAADVVP 271

RESULT 9
QBMGQ1 PRELIMINARY; PRT; 346 AA.
AC Q8MGQ1;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2004 (TREMELrel. 28, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A., Miki A., Williams L.M., Moore Y.F., Geraghty D.E.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF523284; AA74979.1; -
DR EMBL; AF523291; AA74986.1; -
DR EMBL; AF523292; AA74987.1; -
DR EMBL; AY645748; AA73321.1; -
DR EMBL; AY645754; AA73237.1; -
DR HSSP; Q29961; 1HSA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_VHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MECCASSI.
DR ProDom; PD000050; MHC I; 1.
DR SMART; SM00407; IG1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_VHC; 1.
KW Transmembrane.
SQ SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;

Query Match 91.2%; Score 250; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.8e-255;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSHSLRFSFVAVSRPGGEPRIYAVEYDDTQFLRFDSDAAIPRMEPREPWEQSGPYW 60
Db 22 GSHSLRFSFVAVSRPGGEPRIYAVEYDDTQFLRFDSDAAIPRMEPREPWEQSGPYW 81

Qy 61 EWTTGYAKANAQTRVALNRLLRRYNQSEAGSHTLQNMNGCDMGPDRLLRCYHGHAYDG 120
Db 82 EWTTGYAKANAQTRVALNRLLRRYNQSEAGSHTLQNMNGCDMGPDRLLRCYHGHAYDG 141
Qy 121 KDYISLNEDLSRWTAADTVAAITQRFYEAEYAEAEFRTYLEGECLLELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAADTVAAITQRFYEAEYAEAEFRTYLEGECLLELLRRYLENGKETLQ 201

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Qy 181 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Db 202 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 261
Qy 241 FQKWAADVVP 250
Db 262 FQKWAADVVP 271

RESULT 10
Q6DU20 PRELIMINARY; PRT; 346 AA.
AC Q6DU20;
DT 01-OCT-2004 (TREMELrel. 28, Created)
DT 01-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMELrel. 28, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY645755; AA73238.1; -
SQ SEQUENCE 346 AA; 39082 MW; 6F739AA41917E7B2 CRC64;

Query Match 81.8%; Score 224; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.2e-227;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 WVEQGPQYWEWTTGYAKANAQTRVALNRLLRRYNQSEAGSHTLQNMNGCDMGPDRLL 110
Db 72 WVEQGPQYWEWTTGYAKANAQTRVALNRLLRRYNQSEAGSHTLQNMNGCDMGPDRLL 131
Qy 111 RGVHGHAYDGKDYISLNEDLSRWTAADTVAAITQRFYEAEYAEAEFRTYLEGECLLELLRR 170
Db 132 RGVHGHAYDGKDYISLNEDLSRWTAADTVAAITQRFYEAEYAEAEFRTYLEGECLLELLRR 191
Qy 171 YLENGKETLQRADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDEL 230
Db 192 YLENGKETLQRADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDEL 251
Qy 231 VETRPAGDGTFOKWAADVVPVPSGEGQRYTCHVQHEGLPQPLILRW 274
Db 252 VETRPAGDGTFOKWAADVVPVPSGEGQRYTCHVQHEGLPQPLILRW 295

RESULT 11
Q95IT2 PRELIMINARY; PRT; 346 AA.
AC Q95IT2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE MHC class I antigen.
GN Name=Patr-F;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21291697; PubMed=11398964;
RA Adams E.J., Parham P.;
RT "Genomic analysis of common chimpanzee major histocompatibility
complex class I genes.";
RL Immunogenetics 53:200-208(2001).
DR EMBL; AF338355; AAK77479.1; -
DR HSSP; Q29961; 1HSA.

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DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR001039; MHC I.
DR Pfam: PF07654; C1-set; 1.
DR Pfam: PF00129; MHC I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00407; IGcl; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
DR KX Transmembrane.
DR KX SEQUENCE 362 AA; 40625 MW; 39003 MW; 0ECF12B7DB17B814 CRC64;

Query Match
Best Local Similarity 75.9%; Score 208; DB 2; Length 346;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TTGYAKANAQTDRAVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDGKD 122
DB 84 TTGYAKANAQTDRAVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDGKD 143
QY 123 YISLNEDLSRWTAADTVAQITQRFYEAEYAEAEFRTYLEGECLELLRRLYENGKETLQRA 182
DB 144 YISLNEDLSRWTAADTVAQITQRFYEAEYAEAEFRTYLEGECLELLRRLYENGKETLQRA 203
QY 183 DPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTDTELVEPTRPAGDGTQ 242
DB 204 DPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTDTELVEPTRPAGDGTQ 263
QY 243 KWAAVVPSGGEQRYTCHVQHEGLPOPL 270
DB 264 KWAAVVPSGGEQRYTCHVQHEGLPOPL 291

RESULT 12
Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Class Ib.
GN Name=Patr-F;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2709134; PubMed=12799463;
RA Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA Yamagata T., Kuleski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions
RT unavels insertions/deletions as the major path to genomic
RT divergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
DR EMBL: AB100087; BAC78191.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR001039; MHC I.
DR Pfam: PF07654; C1-set; 1.
DR Pfam: PF00129; MHC I; 1.
DR ProDom: PD000050; MHC_I; 1.

Query Match
Best Local Similarity 75.9%; Score 208; DB 2; Length 346;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TTGYAKANAQTDRAVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDGKD 122
DB 84 TTGYAKANAQTDRAVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDGKD 143
QY 123 YISLNEDLSRWTAADTVAQITQRFYEAEYAEAEFRTYLEGECLELLRRLYENGKETLQRA 182
DB 144 YISLNEDLSRWTAADTVAQITQRFYEAEYAEAEFRTYLEGECLELLRRLYENGKETLQRA 203
QY 183 DPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTDTELVEPTRPAGDGTQ 242
DB 204 DPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTDTELVEPTRPAGDGTQ 263
QY 243 KWAAVVPSGGEQRYTCHVQHEGLPOPL 270
DB 264 KWAAVVPSGGEQRYTCHVQHEGLPOPL 291

RESULT 13
Q86OR0 PRELIMINARY; PRT; 254 AA.
AC Q86OR0;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY253271; AAC86775.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR ProDom: PD000050; MHC_I; 1.
DR KX SEQUENCE 254 AA; 28598 MW; C91F225D409AED2 CRC64;

Query Match
Best Local Similarity 66.4%; Score 182; DB 2; Length 254;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRFTSTAVSRPGEGEPRYIAVEYVDDTQPLRFDSDAAIPRMPREFWVEQEGPQYW 60
DB 22 GSHSLRFTSTAVSRPGEGEPRYIAVEYVDDTQPLRFDSDAAIPRMPREFWVEQEGPQYW 81
QY 61 EWTGYAKANAQTDRAVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 120
DB 82 EWTGYAKANAQTDRAVALNRLRRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHAYDG 141
QY 121 KDYISLNEDLSRWTAADTVAQITQRFYEAEYAEAEFRTYLEGECLELLRRLYENGKETLO 180
DB 142 KDYISLNEDLSRWTAADTVAQITQRFYEAEYAEAEFRTYLEGECLELLRRLYENGKETLO 201
QY 181 RA 182
DB 202 RA 203

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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:13:46 : Search time 28.0164 Seconds  
(without alignments)  
941.000 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRVFSTAVSRPGRGEP.....QRYTCHVQHGLPQLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	362	2	A60384
2	126	46.0	345	2	S07114
3	73	26.6	316	2	C37028
4	59	21.5	348	2	S29990
5	44	16.1	275	1	HLHU10
6	44	16.1	298	2	S49994
7	44	16.1	313	2	I36958
8	44	16.1	325	2	I54449
9	44	16.1	332	2	S06424
10	44	16.1	345	2	I68749
11	44	16.1	354	2	I54551
12	44	16.1	357	2	I36966
13	44	16.1	357	2	I36985
14	44	16.1	359	1	HLHU12
15	44	16.1	364	2	S03535
16	44	16.1	365	2	S01171
17	44	16.1	365	2	I36961
18	44	16.1	365	2	I37476
19	44	16.1	365	2	A47636
20	44	16.1	365	2	I83063
21	44	16.1	365	2	I56039
22	44	16.1	365	2	I61856
23	44	16.1	365	2	I37478
24	44	16.1	365	2	I54493
25	44	16.1	365	2	S77963
26	44	16.1	365	2	I38519
27	44	16.1	365	2	I54416
28	44	16.1	365	2	I38518
29	44	16.1	366	1	HLHUW3

30	44	16.1	366	2	I37526	MHC class I histoc
31	44	16.1	366	2	JS0262	class I histocompa
32	44	16.1	366	2	I81232	lymphocyte antigen
33	44	16.1	366	2	I38505	MHC class I histoc
34	44	16.1	366	2	I37544	MHC class I histoc
35	44	16.1	366	2	I81231	lymphocyte antigen
36	44	16.1	366	2	JH0526	MHC class I histoc
37	44	16.1	366	2	I61866	MHC HLA-Cw2.2 chai
38	44	16.1	366	2	I37523	MHC class I histoc
39	44	16.1	366	2	I72113	MHC histocompatibi
40	44	16.1	366	2	I68712	MHC class I histoc
41	44	16.1	366	2	I54283	MHC class I histoc
42	44	16.1	366	2	B37028	MHC class I histoc
43	44	16.1	366	2	I38507	MHC class I histoc
44	44	16.1	366	2	I37527	MHC class I histoc
45	44	16.1	366	2	I37135	MHC class I histoc

#### ALIGNMENTS

##### RESULT 1

A60384  
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C:Accession: A60384; J0147  
Ribury, D.; Epstein, H.; Holmes, N.  
Int. Immunol. 2, 531-537, 1990  
A:Title: The human class I MHC gene HLA-F is expressed in lymphocytes.  
A:Reference number: A60384; MUID:91197689; PMID:1707659  
A:Accession: A60384  
A:Molecule type: DNA  
A:Residues: 1-362 <LUR>  
A:Cross-references: UNIPROT:P30511  
R:Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.  
J. Exp. Med. 171, 1-18, 1990  
A:Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I  
A:Reference number: J0147; MUID:90111605; PMID:1688605  
A:Accession: J0147  
A:Molecule type: DNA  
A:Residues: 1-362 <GER>  
A:Cross-references: DB:X17093; NID:G32223; PIDN:CAA34947.1; PID:G312407  
A:Experimental source: lymphoblastoid cell line  
C:Genetics:  
A:Gene: GDB:HLA-F  
A:Cross-references: GDB:125714  
A:Map position: 6p21.3-6p21.3  
A:Introns: 22/1, 12/1, 204/1, 296/1, 335/1, 346/1, 362/1  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: Glycoprotein; heterodimer; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-111/Domain: alpha-1 <AL1>  
F:78-104/Region: hypervariable  
F:112-203/Domain: alpha-2 <AL2>  
F:164-192/Region: hypervariable  
F:204-295/Domain: alpha-3 <AL3>  
F:217-282/Domain: immunoglobulin homology <IMM>  
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 274; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 1.1e-282;  
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GSHSLRVFSTAVSRPGRGEPRIYAVEYVDVDTQFLRFDSDAAIPRMFPFVWQEGPQYW	60
DB	22	GSHSLRVFSTAVSRPGRGEPRIYAVEYVDVDTQFLRFDSDAAIPRMFPFVWQEGPQYW	81
QY	61	EWTTGYAKANAQTDVRLNLLRRYNOSEAGSTLQGMNGCDMPDGRLLRGVHQHAYDQ	120
DB	82	EWTTGYAKANAQTDVRLNLLRRYNOSEAGSTLQGMNGCDMPDGRLLRGVHQHAYDQ	141
QY	121	KDYISLNEDLSKSTAAADTAQITQRTFYAEAYAEFFTYLEGECLLRLRYLNGKETLQ	180



C:Accession: S44994  
 R:Marget, M.; Brockstedt, D.; Jenisch, S.  
 submitted to the EMBL Data Library, May 1994  
 A:Description: New HLA-Cw6 sequence.  
 A:Reference number: S44994  
 A:Accession: S44994

A:Molecule type: mRNA  
 A:Residues: 1-238 <VAR>  
 A:Cross-references: UNIPROT:Q29866; EMBL:Z33459; NID:G488361; PID:G488361

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:1-72/Domain: signal sequence #status predicted <SIG>  
 F:73-298/Product: class I histocompatibility antigen HLA-Cw6 (fragment) #status predicted  
 F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267  
 |||||  
 DB 248 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 291

## RESULT 7

136958  
 MHC class I chain - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)

C:Date: 02-Jul-1995 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

A:Accession: I36958

R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.

J. Immunol. 142, 3937-3950, 1989

A:Title: Diversity and diversification of HLA-A,B,C alleles.

A:Reference number: I36956; MUID:89235215; PMID:2715640

A:Accession: I36958

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-333 <RES>

A:Cross-references: UNIPROT:Q30989; GB:M24046; NID:G176816; PID:G176817

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:167-232/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267  
 |||||  
 DB 195 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 238

## RESULT 8

154449  
 MHC class I HLA-Cx52 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jan-2000

C:Accession: I54449

R:Takata, H.; Inoko, H.; Ando, A.; Haranaka, M.; Watanabe, B.; Tsuji, K.; Iri, H.

Immunogenetics 28, 265-270, 1988

A:Title: Cloning and analysis of HLA class I cDNA encoding a new HLA-C specificity Cx52.

A:Reference number: I54449; MUID:89330144; PMID:2843461

A:Accession: I54449

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-325 <RES>

A:Cross-references: GB:M21963; NID:G188540; PID:AAA59847.1; PID:G188541

C:Genetics:

A:Gene: GDB:HLA-C

A:Cross-references: GDB:119311; OMIM:142840

A:Map position: gp1.3-gp1.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:179-244/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 325;

Best Local Similarity 100.0%; Pred. No. 2e-38;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267  
 |||||  
 DB 207 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 250

## RESULT 9

S06424  
 MHC class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee

N:Alternate names: MHC Ch1a chain

C:Species: Pan troglodytes (chimpanzee)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S06424; I36959

R:Lawlor, D.A.; Ward, F.B.; Ennis, P.D.; Jackson, A.P.; Parham, P.

Nature 335, 268-271, 1988

A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.

A:Reference number: S06424; MUID:89319000; PMID:3412487

A:Accession: S06424

A:Molecule type: mRNA

A:Residues: 1-332 <LAW>

A:Cross-references: UNIPROT:Q30990

R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.

J. Immunol. 142, 3937-3950, 1989

A:Title: Diversity and diversification of HLA-A,B,C alleles.

A:Reference number: I36956; MUID:89235215; PMID:2715640

A:Accession: I36959

A:Molecule type: mRNA

A:Residues: 1-332 <RES>

A:Cross-references: GB:M24047; NID:G176818; PID:AAA35426.1; PID:G553155

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; membrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-114/Domain: alpha-1 #status predicted <EX1>

F:115-206/Domain: alpha-2 #status predicted <EX2>

F:220-285/Domain: immunoglobulin homology <IMM>

F:307-331/Domain: transmembrane #status predicted <TM>

F:110/Binding site: carbohydrate (asn) (covalent) #status predicted

F:125-188,227-232/Disulfide bonds: #status predicted

Query Match 16.1%; Score 44; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 2e-38;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267  
 |||||  
 DB 248 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 291

## RESULT 10

I68749  
 MHC class I lymphocyte antigen - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004

C:Accession: I68749

R:Pohl, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.

Immunogenetics 29, 297-307, 1989

A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B

A:Reference number: I54457; MUID:89233295; PMID:2714852

A:Accession: I68749

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-345 <RES>

A:Cross-references: UNIPROT:Q29963; GB:M28206; NID:G576476; PID:AAA57258.1; PID:G576477

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:199-264/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-38;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267



F;219-284/Domain: immunoglobulin homology <IMM>  
 F;298-336/Domain: transmembrane #status predicted <TM>  
 F;337-364/Domain: intracellular #status predicted <INT>

Query Match 16.1%; Score 44; DB 2; Length 364;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-38;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTQKWAAVVVPSSGEQRYTCHVQHEGLP 267  
 |||||  
 Db 247 QTQDTLVETRPAGDGTQKWAAVVVPSSGEQRYTCHVQHEGLP 290  
 |||||

Search completed: December 15, 2004, 18:25:17  
 Job time : 29.0164 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 18:14:01, Search time 30.818 Seconds  
(without alignments)  
589.627 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 274  
Sequence: 1 GSHSLRYFSTAVSRGGRGP.....QRYTCHVQHEGLPQPLILRW 274

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size: 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/6CTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	36.1	120	4	US-09-513-999C-4290
2	44	15.1	274	1	US-08-222-851-1
3	39	14.2	117	2	US-08-486-057-9
4	39	14.2	117	3	US-08-958-316-9
5	39	14.2	145	2	US-08-406-057-8
6	39	14.2	145	3	US-08-958-316-8
7	30	10.9	289	2	US-08-484-905-79
8	30	10.9	289	3	US-08-481-985B-79
9	30	10.9	289	3	US-08-370-476-79
10	29	10.6	274	2	US-08-484-905-105
11	29	10.6	274	2	US-08-484-905-107
12	29	10.6	274	2	US-08-484-905-108
13	29	10.6	274	3	US-08-481-985B-105
14	29	10.6	274	3	US-08-481-985B-107
15	29	10.6	274	3	US-08-481-985B-108
16	29	10.6	274	3	US-08-370-476-105
17	29	10.6	274	3	US-08-370-476-107
18	29	10.6	274	3	US-08-370-476-108
19	29	10.6	341	3	US-08-890-719-38
20	29	10.6	365	2	US-08-484-905-97
21	29	10.6	365	2	US-08-484-905-98
22	29	10.6	365	2	US-08-484-905-99
23	29	10.6	365	2	US-08-484-905-100
24	29	10.6	365	2	US-08-484-905-101
25	29	10.6	365	2	US-08-481-985B-97
26	29	10.6	365	3	US-08-481-985B-98
27	29	10.6	365	3	US-08-481-985B-99

28 29 10.6 365 3 US-08-481-985B-100 Sequence 100, App  
29 29 10.6 365 3 US-08-481-985B-101 Sequence 101, App  
30 29 10.6 365 3 US-08-652-265-23 Sequence 23, App  
31 29 10.6 365 3 US-08-834-497A-23 Sequence 23, App  
32 29 10.6 365 3 US-08-370-476-97 Sequence 97, App  
33 29 10.6 365 3 US-08-370-476-98 Sequence 98, App  
34 29 10.6 365 3 US-08-370-476-99 Sequence 99, App  
35 29 10.6 365 3 US-08-370-476-100 Sequence 100, App  
36 29 10.6 365 3 US-08-370-476-101 Sequence 101, App  
37 29 10.6 365 3 US-09-503-444A-23 Sequence 23, App  
38 27 9.9 184 2 US-08-484-905-83 Sequence 83, App  
39 27 9.9 184 2 US-08-481-985B-83 Sequence 83, App  
40 27 9.9 184 2 US-08-370-476-83 Sequence 83, App  
41 25 9.1 108 2 US-08-484-905-82 Sequence 82, App  
42 25 9.1 108 3 US-08-481-985B-82 Sequence 82, App  
43 25 9.1 108 3 US-08-370-476-82 Sequence 82, App  
44 25 9.1 290 2 US-08-484-905-80 Sequence 80, App  
45 25 9.1 290 3 US-08-481-985B-80 Sequence 80, App

#### ALIGNMENTS

RESULT 1  
US-09-513-999C-4290  
; Sequence 4290, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4290  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -17..-1  
; OTHER INFORMATION: score 9.3  
; OTHER INFORMATION: seq SLILLLSGALALT/DT

US-09-513-999C-4290  
Query Match 36.1%; Score 99; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 28-90;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGRGPYAVYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQY 60  
DB 22 GSHSLRYFSTAVSRGGRGPYAVYVDDTQFLRFDSDAAIPRMEPRPWPVEQGPQY 81

QY 61 EWTTGYAKAQTDRVALNLLRRYVQSEAGSHTLQGMN 99  
DB 82 EWTTGYAKAQTDRVALNLLRRYVQSEAGSHTLQGMN 120

RESULT 2  
US-08-222-851-1  
; Sequence 1, Application US/08222851  
; Patent No. 5723128  
; GENERAL INFORMATION:  
; APPLICANT: CLAYBERGER, CAROL A.  
; APPLICANT: KRENSKY, ALAN M.  
; APPLICANT: PARHAM, PETER  
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")

;; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES  
;; NUMBER OF SEQUENCES: 43  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
;; CITY: WASHINGTON  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20006-1812  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/222,851  
;; FILING DATE: 05-APR-1994  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MILLMAN, ROBERT A.  
;; REGISTRATION NUMBER: 36,217  
;; REFERENCE/DOCKET NUMBER: 28600-20200.22  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 494-0792  
;; TELEX: 90-4030 MRSNFOERSWGH  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 274 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
US-08-222-851-1

Query Match 16.1%; Score 44; DB 1; Length 274;  
Best Local Similarity 100.0%; Pred. No. 1.5e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQTELVETRPAGDGTGFKWAAVVPSGEQRYTCHVOHEGLP 267  
DB 224 QTQTELVETRPAGDGTGFKWAAVVPSGEQRYTCHVOHEGLP 267

RESULT 3  
US-08-406-057-9  
; Sequence 9, Application US/08406057  
; Patent No. 5856442  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/406,057  
; FILING DATE: 17-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94 03179

;; FILING DATE: 18-MAR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OBLON, NORMAN F  
;; REGISTRATION NUMBER: 24,618  
;; REFERENCE/DOCKET NUMBER: 846-331-0  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 413-3000  
;; TELEFAX: (703) 413-2220  
;; TELEX: 248855 OPAT UR  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 117 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;;  
US-08-406-057-9

Query Match 14.2%; Score 39; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 6.3e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTGFKWAAVVPSGEQRYTCHVOHEGLP 267  
DB 51 ELVETRPAGDGTGFKWAAVVPSGEQRYTCHVOHEGLP 89

RESULT 4  
US-08-958-316-9  
; Sequence 9, Application US/08958316  
; Patent No. 6231659  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 2202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Tape  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/958,316  
; FILING DATE: 27-OCT-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94 03179  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 0846-0437-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-958-316-9

Query Match 14.2%; Score 39; DB 3; Length 117;  
Best Local Similarity 100.0%; Pred. No. 6.3e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 267  
Db 51 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 89

## RESULT 5

US-08-406-057-8  
; Sequence 8, Application US/08406057  
; Patent No. 5856442  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 2202

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406.057  
FILING DATE: 17-MAR-1995  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 846-331-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-406-057-8

Query Match 14.2%; Score 39; DB 2; Length 145;  
Best Local Similarity 100.0%; Pred. No. 7.6e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 267  
Db 79 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 117

## RESULT 6

US-08-958-316-8  
; Sequence 8, Application US/08958316  
; Patent No. 6291659  
; GENERAL INFORMATION:

APPLICANT: CAROSELLA, EDGARDO D  
APPLICANT: MOREAU, PHILIPPE  
APPLICANT: GLUCKMAN, ELIANE  
APPLICANT: KIRSZENBAUM, MAREK  
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 2202

## COMPUTER READABLE FORM:

MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958.316  
FILING DATE: 27-OCT-1997  
CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 0846-0437-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-958-316-8

Query Match 14.2%; Score 39; DB 3; Length 145;  
Best Local Similarity 100.0%; Pred. No. 7.6e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 267  
Db 79 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 117

## RESULT 7

US-08-484-905-79  
; Sequence 79, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:

APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
Complex (MHC) Determinant and Methods for Using the  
Complex (MHC) Determinant  
TITLE OF INVENTION: Determinant  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
ZIP: 20005-3315

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-79

Query Match 10.9%; Score 30; DB 2; Length 289;
Best Local Similarity 100.0%; Pred.No.1.2e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTELVTETPAGDGTFOKWAIVVPSGEEQ 255
DB 226 QDTELVTETPAGDGTFOKWAIVVPSGEEQ 255

RESULT 8
US-08-481-985B-79
; Sequence 79, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; DUNNEE
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991

```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-985B-79

Query Match 10.9%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred.No.1.2e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTELVTETPAGDGTFOKWAIVVPSGEEQ 255
DB 226 QDTELVTETPAGDGTFOKWAIVVPSGEEQ 255

RESULT 9
US-08-370-476-79
; Sequence 79, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ocius, David
; APPLICANT: Casrouge, Armanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; DUNNEE
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400

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INFORMATION FOR SEQ ID NO: 79;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-370-476-79

Query Match 10.6%; Score 30; DB 3; Length 289;  
Best Local Similarity 100.0%; Pred. No. 1.1e-21;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 QTELVETRPAGDGTFOKWAIVVPSGREQ 255  
Db 226 QTELVETRPAGDGTFOKWAIVVPSGREQ 255

## RESULT 10

US-08-484-905-105  
Sequence 105, Application US/08484905  
Patent No. 5976551  
GENERAL INFORMATION:

APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
Determinant and Methods for Using the  
Determinant

TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the  
Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS: 127

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS-/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,905

FILING DATE: 07-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 03495.0106-03000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 274 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-105

Query Match 10.6%; Score 29; DB 2; Length 274;  
Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTELVETRPAGDGTFOKWAIVVPSG 252

Db 224 QTELVETRPAGDGTFOKWAIVVPSG 252

## RESULT 11

US-08-484-905-107  
Sequence 107, Application US/08484905  
Patent No. 5976551  
GENERAL INFORMATION:

APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe

TITLE OF INVENTION: An Altered Major Histocompatibility

Determinant and Methods for Using the

Determinant

TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the

Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS-/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,905

FILING DATE: 07-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 03495.0106-03000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 274 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-107

Query Match 10.6%; Score 29; DB 2; Length 274;  
Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTELVETRPAGDGTFOKWAIVVPSG 252

Db 224 QTELVETRPAGDGTFOKWAIVVPSG 252

## RESULT 12

US-08-484-905-108  
Sequence 108, Application US/08484905  
Patent No. 5976551  
GENERAL INFORMATION:

APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe

TITLE OF INVENTION: An Altered Major Histocompatibility

Determinant and Methods for Using the

Determinant

Query Match 10.6%; Score 29; DB 2; Length 274;  
Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTELVETRPAGDGTFOKWAIVVPSG 252

```
/ TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
/ TITLE OF INVENTION: Determinant
/ NUMBER OF SEQUENCES: 127
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ DUNN
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,905
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/801,818
/ FILING DATE: 05-DEC-1991
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/792,473
/ FILING DATE: 15-NOV-1991
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E. R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 03495.0106-03000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4400
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 108:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 274 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-484-905-108

Query Match 10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLVETRPAGDGTFOKWAIVVPSG 252
Db 224 QTQDTLVETRPAGDGTFOKWAIVVPSG 252

RESULT 13
US-08-481-985B-105
/ Sequence 105, Application US/08481985B
/ Patent No. 6011146
/ GENERAL INFORMATION:
/ APPLICANT: Mottez, Estelle
/ APPLICANT: Abastado, Jean-Pierre
/ APPLICANT: Kourilsky, Philippe
/ TITLE OF INVENTION: Altered Major Histocompatibility Complex
/ NUMBER OF SEQUENCES: 148
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ DUNN
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 148
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/801,818
/ FILING DATE: 05-DEC-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/792,473
/ FILING DATE: 15-NOV-1991
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ PC-DOS/MS-DOS
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/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,985B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/801,818
/ FILING DATE: 05-DEC-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/792,473
/ FILING DATE: 15-NOV-1991
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meyers, Kenneth J.
/ REGISTRATION NUMBER: 25,146
/ REFERENCE/DOCKET NUMBER: 03495.0106-04000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4400
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 105:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 274 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-481-985B-105

Query Match 10.6%; Score 29; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLVETRPAGDGTFOKWAIVVPSG 252
Db 224 QTQDTLVETRPAGDGTFOKWAIVVPSG 252

RESULT 14
US-08-481-985B-107
/ Sequence 107, Application US/08481985B
/ Patent No. 6011146
/ GENERAL INFORMATION:
/ APPLICANT: Mottez, Estelle
/ APPLICANT: Abastado, Jean-Pierre
/ APPLICANT: Kourilsky, Philippe
/ TITLE OF INVENTION: Altered Major Histocompatibility Complex
/ NUMBER OF SEQUENCES: 148
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ DUNN
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,985B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/801,818
/ FILING DATE: 05-DEC-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/792,473
/ FILING DATE: 15-NOV-1991
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
```

NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0106-04000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 107:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 274 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-481-985B-107

Query Match 10.6%; Score 29; DB 3; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTQKWAAVVPSG 252  
 DB 224 QTQDTLVETRPAGDGTQKWAAVVPSG 252

RESULT 15

US-08-481-985B-108  
 Sequence 108, Application US/08481985B  
 Patent No. 6011146  
 GENERAL INFORMATION:  
 APPLICANT: Mottez, Estelle  
 APPLICANT: Abastado, Jean-Pierre  
 APPLICANT: Kourilsky, Philippe  
 TITLE OF INVENTION: Altered Major Histocompatibility Complex  
 NUMBER OF SEQUENCES: 148  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &  
 ADDRESSES: Dunner  
 STREET: 1300 I Street, N.W., Suite 700  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005-3315  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/481.985B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/801,818  
 FILING DATE: 05-DEC-1991  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/792,473  
 FILING DATE: 15-NOV-1991  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 03495.0106-04000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 274 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-481-985B-108

Query Match 10.6%; Score 29; DB 3; Length 274;  
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 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 224 QTQDTLVETRPAGDGTQKWAAVVPSG 252  
 Search completed: December 15, 2004, 18:26:18  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 12:02:13 ; Search time 5019 Seconds  
(without alignments)  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 8: gb\_pl.\*
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- 10: gb\_ro.\*
- 11: gb\_ats.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1089	100.0	1089	6	E63813	E63813 Cancer cell
3	1089	100.0	1089	6	AX52555	AX52555 Sequence
4	1089	100.0	1188	6	CQ776417	CQ776417 Sequence
5	1089	100.0	1188	6	CQ776511	CQ776511 Sequence
6	1037	95.2	1041	9	AY253270	AY253270 Homo sapi
7	986	90.5	1041	9	AY253269	AY253269 Homo sapi
8	986	90.5	1167	9	BC062991	BC062991 Homo sapi
9	985	90.4	1523	9	BC003260	BC003260 Homo sapi
10	927	85.1	2598	9	AK096962	AK096962 Homo sapi
11	921	84.6	972	9	AY216682	AY216682 Homo sapi
12	921	84.6	972	9	AY221102	AY221102 Homo sapi
13	822	75.5	822	6	BD187422	BD187422 Cancer pr
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18	645	59.2	645	6	E63815	E63815 Cancer cell
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35	279	25.6	6941	9	AY645749	Homo sapi
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37	279	25.6	6956	9	AY645745	Homo sapi
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39	279	25.6	6967	9	AF523294	Homo sapi
40	279	25.6	6968	9	AY645742	Homo sapi
41	279	25.6	6968	9	AY645747	Homo sapi
42	279	25.6	6968	9	AY645751	Homo sapi
43	279	25.6	6968	9	AY645752	Homo sapi
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## ALIGNMENTS

RESULT 1	BD187421	1089 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD187421				
DEFINITION	Cancer prophylactic/treatment agent.				
ACCESSION	BD187421				
VERSION	BD187421.1				
KEYWORDS	JP 2003012544-A/1.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1089)				
AUTHORS	Egawa, K.				
TITLE	Cancer prophylactic/treatment agent				
JOURNAL	Patent: JP 2003012544-A 1 15-JAN-2003;				
COMMENT	K EGAWA et al				
	OS human				
	PN JP 2003012544-A/1				
	PD 15-JAN-2003				
	PF 27-MAR-2002 JP 2002088991				
	PI koji egawa				
	CC				

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Query Match	100.0%;	Score 1089; DB 6; Length 1089;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches 1089;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
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Db	1	ATGCGGCGCCGAGAGCTCCTCCTCGCTGCTCTCAGGGGCGCTGGCCCTGACCGATCTTGG 60
Qy	61	GCGGGCTCCACCTCTCTTGAGTATTTTCAGACCGCTGTGTGCGGGCCCGCGCGGGAG 120
Db	61	GCGGGCTCCACCTCTCTTGAGTATTTTCAGACCGCTGTGTGCGGGCCCGCGCGGGAG 120



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Db      481  GCTCAGATCACCCAGCGCTTCTATGAGCAGAGGAAATATGAGAGGAGTTCCAGGACCTAC 540
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Db      541  CTGGAGGGGAGTCCCTGGAGTGTCTCCSCAGATACCTTGGAGAAATGGAGAGACGCTA 600
Qy      601  CAGCGGCGAGATCTCTCAAGGACACACGTTGGTCCACACCCAGTCTCTGACCATGAGGCC 660
Db      601  CAGCGGCGAGATCTCTCAAGGACACACGTTGGTCCACACCCAGTCTCTGACCATGAGGCC 660
Qy      661  ACCCTGAGTGTCTGGGCGCTTCTACCTCTGGGAGATCAACGCTGAGGAGATCAACGCTGAGGAG 720
Db      661  ACCCTGAGTGTCTGGGCGCTTCTACCTCTGGGAGATCAACGCTGAGGAGATCAACGCTGAGGAG 720
Qy      721  GATGGGAGGAGACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGAGGGGATGGA 780
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Qy      781  ACCTTCCAGAAGTGGGCGCTTGTGGTGTCTTCTGGAGAGGAAACAGAGATACACATGC 840
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Qy      1081  AAAGTGTGA 1089
Db      1081  AAAGTGTGA 1089

RESULT 3
AX552555
LOCUS      AX552555
DEFINITION Sequence 1 from Patent EP1245675.
ACCESSION AX552555
VERSION    AX552555.1 GI:25896575
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Egawa, K.
TITLE      Cancer cell-specific hla-f antigen and a diagnostic method of
            cancer by using thereof
JOURNAL    Patent: EP 1245675-A.1 02-OCT-2002;
            Egawa, Kohji (JP); Medinet Co., Ltd. (JP); Kimura, Yoshiji (JP)
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGCGCCCGAAGCCTCTCTGCTGCTCTCAGGGGCGCTTGGCCCTGACGATACTTGG 60

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Qy      481  GCTCAGATCAACCGCTTCTATGAGGACAGAGGAAATATGAGAGAGTTCAGGACCTAC 540
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Qy      601  CAGCGCGCAGATCTCTCAAGGACACAGTTGCCACACCCATCTCTCAGCATGAGGCC 660
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LOCUS	AY253270				
DEFINITION	Human epsilon MHC class II allele, complete cds.				
ACCESSION	AY253270				
VERSION	AY253270.1				
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KEYWORDS
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    Homo sapiens (human)
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    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    He X., Xu, L., Liu Y. and Zeng Y.
  TITLE
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    He X., Xu, L., Liu Y. and Zeng, Y.
    Direct Submission
    Submitted (08-MAR-2003) Key Laboratory of Ministry of Education for
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QY	181	CGCGGATTCGAGGATGGAGCGCGGGAGCCGTGGGTGGAGCAAGAGGGGCCCGACGAT	240	
Db	181	CGCGGATTCGAGGATGGAGCGCGGGAGCCGTGGGTGGAGCAAGAGGGGCCCGACGAT	240	
QY	241	TGGAGTGGACCAAGGTCAGGCGCAAGCGCACAGACTGACCGAGTGGCCCTGAGG	300	
Db	241	TGGAGTGGACCAAGGTCAGGCGCAAGCGCACAGACTGACCGAGTGGCCCTGAGG	300	
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Db	301	AACCTGCTCCGCGCTACACAGAGCGAGGCTGGGTCTCACCCCTCCAGGGGAATGAAT	360	
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 Qy 841 CATGTCAGACAGAGGGGCTGCCAGCCCTCATCTGATGATGAGAGGAGCTCTCCCGAG 900  
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 Qy 1021 TACTCTCAGGCTGCAGT 1037  
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## RESULT 8

BC062991

LOCUS

DEFINITION

Homo sapiens major histocompatibility complex, class I, F, mRNA

(CDNA clone MGC:74962 IMAGE:5496696), complete cds.

ACCSSION

BC062991

VERSION

MGC:74962

KEYWORDS

MGC:74962

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenman, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Hellon, E., Kettner, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smal, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

REMARK

COMMENT

2 (bases 1 to 1167)

Straussberg, R.

Direct Submission

Submitted (01-DEC-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cga@nci.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc\_mgc@hgr.nih.gov

Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W.,

Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H., and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: INAK Plate: 135 Row: 0 Column: 19

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 9665231.

Location/Qualifiers

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AQTRQYEAAYAEFRYIEGCELLRLRYLNGKTLQADPPKARVAHPISD

EATLRWALGFYPAEITLTWQDEGTQTLVETRFAGDGTQKAAVAVVPSGEQ

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58. 604

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/note="MHC I; Region: Class I Histocompatibility antigen,

domains alpha 1 and 2"

/db\_xref="CDD:pfam00129"

617. 892

/gene="HLA-F"

/note="IGC; Region: Immunoglobulin domain constant region

subfamily"

/db\_xref="CDD:cd00098"

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ORIGIN



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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Query Match 90.4%; Score 985; DB 9; Length 1523;
Best Local Similarity 99.9%; Pred. No. 0;
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Qy 661 ACCCTGAGGTGCTGGGCGCTTCTACCTTGGGAGATCAGCTGACCTGAGCGAGCGG 720
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Qy 721 CATGGCAGGAAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCTTGGAGGAGATGGA 780
Db 777 GATGGCAGGAAACAGACCCAGGACACAGAGCTTGTGGAGACCCAGGCTTGGAGGAGATGGA 836
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Db 1077 TACTCTCAGGCTGCAG 1092

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RESULT 10
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LOCUS
DEFINITION
AK096962.1 GI:21756582
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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AK096962 2598 bp mRNA linear PRI 30-JAN-2004
to HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN P. PRECURSOR.
AK096962.1 GI:21756582
Oligo capping; full insert sequence.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohbayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Takahara, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Taira, K., Tanaka, K., Tanai, H., Kimura, M., Watanabe, M.,
Muraoka, S., Chiba, T., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
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Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,
Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shichata, N., Sano, S., Motiya, S., Momiyama, H., Satoh, N., Takami, S.,
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Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
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Qy	904	ACCATCCCAATCGTGGGCATCGTTGTGGCCCTGTGTCCTTGGAGCTGTGGTCACTGGA	963
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Qy	964	GCTGTGGTCGCTGCTGTGATG	984
Db	952	GCTGTGGTCGCTGCTGTGATG	972

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LOCUS	AY221102	972 bp	mRNA	linear	PRI 08-FEB-2003
DEFINITION	Homo sapiens MHC class I antigen (HLA-F)			mRNA, partial cds.	

ACCESSION	AY221102
VERSION	AY221102.1
	GI:28274639

KEYWORDS  
Homo sapiens (human)  
SOURCE

ORGANISM	Homo sapiens
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:	

REFERENCE  
1 (bases 1 to 972)  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

**AUTHORS**  
Liu, Y., Xu, L., Zeng, Y. and He, X.  
1 (cases 1 to 3/2).  
A new polymorphism in non-classical virus class I virus.

JOURNAL  
Unpublished  
A new polymorphism in non-classical MAC class I HLA-F  
11111

2 (pages 1 to 9/2)

REFERENCE

AUTHORS

Liu, Y., Xu, L., Zeng, Y. and He, X.

**JOURNAL TITLE** Direct Submission  
Submitted (20-JAN-2003) Key Laboratory of Ministry of Education for

Tissue Transplantation and Immunology, Jinan University, Shipai,  
Guangzhou, Guangdong 510632, China

FEATURES	Location/Qualifiers
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QRFYEAEEYAEBFRTYLBEGCELELLRRYLNGKETLQRADPPKRAHVAAHPIISDHEATL  
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252  
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DB 61 TCCTTGAGGTATTTACGACACCGCTGTGTCCGGCCCGGGGAGCCCCGCTACATC 120

133 GCGGTGGAGTACGTACGACGACAGCAATTCTTGGCGTTCGACAGCGACGCCGGGATTCG 192

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:01 11 November 2014

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121 GCGTGGAGTACGTAGACGACAGCAATTCCTCGGTTTCGACAGCGCCGCGATTCCG 180
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361 GGGGCCGACGACGCGCTCCCTCCGCGGTATCACACGACGCGGTACGACGCGCAAGATTAC 420
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733 CAGACCCAGGACACAGAGCTTGTGGACACAGCGCTTCAGGGGATGGAACTTCCAGAG 792
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793 TGGGCGCTTGGCTTCTACCTCGGAGATCACGCTGACCTGGAGGGGATGGAGGAC 852
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853 GAGGGGCTGCCAGCGCCCTCATCTGAGATGGAGGAGTCTCCCGAGCCACCATCCCC 912
841 GAGGGGCTGCCAGCGCCCTCATCTGAGATGGAGGAGTCTCCCGAGCCACCATCCCC 900
913 ATCGTGGGATCGTGTGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 972
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961 GCTGCTGTGATG 972

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RESULT 13
BD187422
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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BD187422  
Cancer prophylactic/treatment agent.  
BD187422  
GI:32997161  
JP 2003012544-A/2.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 822)  
Egawa,K.

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TITLE      Cancer prophylactic/treatment agent
JOURNAL    Patent: JP 2003012544-A 2 15-JAN-2003;
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COMMENT    OS human
           PN JP 2003012544-A/2
           PD 15-JAN-2003
           PF 27-MAR-2002 JP 2002088991
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           CC
           FH
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Best Local Similarity 100.0%; Pred. No. 0;
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Qy 124 CGCTACATCGCGGTGAGTACGTAGACGACACGCAATTCCTGGGTTTCGACACGCGACGCC 183
Db 61 CGCTACATCGCGGTGAGTACGTAGACGACACGCAATTCCTGGGTTTCGACACGCGACGCC 120
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Db 121 GCGATTCGAGATCGAGCCCGGAGCCGTGGTGGAGCAAGAGGGGCGCGAGTATGG 180
Qy 244 GAGTGACACAGGGTACGCGCAAGCGCAACGACAGACTGACGAGTGGCCCTGAGGAAC 303
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Qy 364 TGGCATGGGCGCCGAGCGAGCGCTCTCCGCGGTATCACAGCAGCGGTACGACGCC 423
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E63814
LOCUS 822 bp DNA linear PAT 27-AUG-2002
DEFINITION Cancer cell-specific HLA-F antigen and method for diagnosing cancer
using the same.
ACCESSION E63814
VERSION E63814.1 GI:2253652
KEYWORDS JP 2001095584-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Egawa,K.
JOURNAL Cancer cell-specific HLA-F antigen and method for diagnosing cancer
COMMENT Patent: JP 2001095584-A 2 10-APR-2001;
OS Homo sapiens (human)
PN JP 2001095584-A/2
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279566
PI KOJI EGAWA
PC C12N15/09,C07K14/82,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/PC
02,
PC G01N33/53,G01N33/574,G01N33/68//(C12N1/21,C12R1:19),(C12P21/02,PC
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CC C12N15/00,C12N5/00
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Best Local Similarity 100.0%; Pred.No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 GGCTCCCACTCTTGAGGTATTTTCAGCACCGCTGTGCGCGCCCGCGCGGGAGGCC 123
Db 1 GGCTCCCACTCTTGAGGTATTTTCAGCACCGCTGTGCGCGCCCGCGCGGGAGGCC 60
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QY 724 GGGAGGACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTCCAGGGATGGAACC 783
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QY 784 TTCCAGAAAGTGGGCGCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 843
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QY 844 GTGACAGCAGAGGGGCTGCCCGAGCCCTCATCTGAGATGG 885
Db 781 GTGACAGCAGAGGGGCTGCCCGAGCCCTCATCTGAGATGG 822

RESULT 15
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LOCUS 822 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 2 from Patent EP1245675.
ACCESSION AX552556
VERSION AX552556.1 GI:25896576
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Egawa,K.
TITLE Cancer cell-specific hla-f antigen and a diagnostic method of
cancer by using thereof
JOURNAL Patent: EP 1245675-A 2 02-OCT-2002;
Egawa, Kohji (JP) ; Medinet Co., Ltd. (JP) ; Kimura, Yoshiji (JP)
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred.No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 GGCTCCCACTCTTGAGGTATTTTCAGCACCGCTGTGCGCGCCCGCGCGGGAGGCC 123
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QY 184 GCGATTCCGAGTGGAGCGCGGGAGCGGTGGTGGAGCAAGAGGGCGCGCGAGTATGG 243
Db 121 GCGATTCCGAGTGGAGCGCGGGAGCGGTGGTGGAGCAAGAGGGCGCGCGAGTATGG 180
QY 244 GAGTGACACAGGGTACGCCAGGCGCAACCGACAGACTGACCGAGTGGCGCTTGAGGAAC 303

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Qy	424		AAGGATTACATCTCCCTGAACAGAGGACCTGGCTCTTGACCCCGCGGACACCGTGGCT	483
Db	361		AAGGATTACATCTCCCTGAACAGAGGACCTGGCTCTTGACCCCGCGGACACCGTGGCT	420
Qy	484		CAGATCACCCAGCGCTTCTATGAGGACAGAGGATATGCAGAGGAGTTTCAGGACCTACCTG	543
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Qy	544		GAGGCGAGTGCTTGGAGTTGCTCCGACAGATCTTCGAGAAATGGGAAAGGAGACGCTACAG	603
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Qy	604		CGGCGAGATCTCCAAAGGCACACGTTGCCACACCCCATCTCTGACCATGAGGCCACC	663
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Qy	664		CTGAGGTGCTGGGCCCTGGGCTTCTACCTTGGGAGATCACGCTGACCTGGGAGCGGAT	723
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Qy	724		GGGAGGAAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCTGCGAGGGATGGAACC	783
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Db	781		GTGAGCACAGAGGGGCTGCCCGCCCTCATCTCAGATGG	822

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OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 12: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1089	100.0	1089	10	ADP55584	ADP55584 DNA encod
3	1089	100.0	1188	12	ADJ74945	ADJ74945 Marker ge
4	1089	100.0	1188	12	ADJ74851	ADJ74851 Marker ge
5	1089	100.0	1188	12	ADP10447	ADP10447 Reference
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7	952	87.4	2037	5	AAS90740	AAS90740 DNA encod
8	952	87.4	2037	5	ADI21449	ADI21449 Novel hum
9	822	75.5	822	4	AH45556	AH45556 Human can
10	822	75.5	822	10	ADP55585	ADP55585 DNA encod
11	785	72.2	816	3	AACT78195	AACT78195 Human can
12	645	59.2	645	4	AH45557	AH45557 Human can
13	645	59.2	645	10	ADP55586	ADP55586 DNA encod
14	361	33.1	424	3	AACT00215	AACT00215 Human sec
15	355	32.6	487	9	ACH50642	ACH50642 Human mam
16	339	31.1	459	10	ABX74535	ABX74535 Human cDN
17	289	26.5	1096	10	ADI21922	ADI21922 Novel hum
18	279	25.6	4316	5	ABA83122	ABA83122 HLA-Cw ov
19	279	25.6	4316	5	ABN97218	ABN97218 Gene #371
20	279	25.6	4316	10	ABX3954	ABX3954 HLA-F gen
21	277	25.4	3098	4	AAR86871	AAR86871 Human imm

22	277	25.4	3098	4	AA104024	AA104024 Human rep
23	277	25.4	3098	5	AB18125	AB18125 Human ner
24	277	25.4	3098	5	AAS40421	AAS40421 DNA encod
25	277	25.4	148934	6	ABR83570	ABR83570 Human cDN
26	276	25.3	546	12	ADQ21922	ADQ21922 Human sof
27	272	25.0	907	2	AAZ53005	AAZ53005 Human pro
28	228	20.9	289	12	ACH84959	ACH84959 Human gen
29	228	20.9	552	12	ACH71259	ACH71259 Human gen
30	212	19.5	1414	5	AAS93415	AAS93415 DNA encod
31	104	9.6	240	2	AAT23311	AAT23311 Human gen
32	89	8.2	379	4	AA190453	AA190453 Human pol
33	85	7.8	561	6	ABQ56008	ABQ56008 Human ova
34	73	6.7	274	3	AA394614	AA394614 HLA-B gen
35	73	6.7	301	4	ABA21426	ABA21426 Probe #11
36	73	6.7	301	4	ABA66506	ABA66506 Human toe
37	73	6.7	301	4	ABA146715	ABA146715 Probe #15
38	73	6.7	301	4	ABA48596	ABA48596 Human bre
39	73	6.7	301	4	ABA33570	ABA33570 Probe #12
40	73	6.7	301	4	AAK40662	AAK40662 Human bon
41	73	6.7	301	4	AAK14929	AAK14929 Human liv
42	73	6.7	301	4	ABS40231	ABS40231 Human liv
43	73	6.7	301	5	AA107121	AA107121 Probe #71
44	73	6.7	301	6	ABS14623	ABS14623 Human gen
45	73	6.7	332	4	AAK54319	AAK54319 Human hae

ALIGNMENTS

RESULT 1  
AAH45555  
ID AAH45555 standard; DNA; 1089 BP.  
XX  
AC AAH45555;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 1.  
XX  
KW HLA-F antigen; cancer cell specific; human; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key  
CDS Location/Qualifiers  
FT 1..1089  
FT /\*tag= a  
FT /product= "Cancer cell specific HLA-F antigen"  
XX  
PN JP2001095584-A.  
XX  
PD 10-APR-2001.  
XX  
PF 30-SEP-1999; 99JP-00279566.  
XX  
PR 30-SEP-1999; 99JP-00279566.  
XX  
PA (EGAW/) EGAWA K.  
PA (MEDI-) MEDINET KK.  
PA (KIMU/) KIMURA K.  
XX  
WPI; 2001-360493/38.  
P-PSDB; AAG64617.  
XX  
PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
XX  
PS Claim 3; Page 8-9; 12pp; Japanese.  
XX  
CC This invention relates to a cancer cell specific HLA-F antigen. The  
CC invention includes DNA encoding the antigen, and a method for the  
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
CC used in a method to diagnose cancer, in which the protein is used to  
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
CC sequence represents DNA encoding the cancer cell-specific HLA-F antigen

















Db 721 TTCAGAGTGGCGCTGTGGTGGCTTCTGGAGAGGACAGAGATACATGCCAT 780  
 Qy 844 GTGAGAGTGGCGCTGTGGTGGCTTCTGGAGAGGACAGAGATACATGCCAT 780  
 Db 781 GTGAGAGTGGCGCTGTGGTGGCTTCTGGAGAGGACAGAGATACATGCCAT 780

RESULT 10  
 ADF55585  
 ID ADF55585 standard; DNA; 822 BP.  
 AC ADF55585;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE DNA encoding fragment #1 of human cancer-cell specific HLA-F antigen.  
 XX  
 KW Cancer; human leukocyte antigen-F; HLA-F;  
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
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 FT 1..822  
 FT CDS /tag=a  
 FT partial  
 FT /note="This sequence lacks both start and stop codons"  
 XX  
 PN JP2003012544-A.  
 XX  
 PD 15-JAN-2003.  
 XX  
 PF 27-MAR-2002; 2002JP-00089991.  
 XX  
 PR 27-MAR-2001; 2001JP-00090121.  
 XX  
 PA (EGAW/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU/) KIMURA Y.  
 XX  
 DR WPI: 2003-486263/46.  
 DR P-PSDB; ADF55588.  
 XX  
 PT Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
 XX  
 PS Disclosure; SEQ ID NO 2; 19pp; Japanese.  
 XX  
 CC The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence encodes part of the human cancer-cell specific HLA-F antigen.  
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 SQ Sequence 822 BP; 174 A; 250 C; 273 G; 125 T; 0 U; 0 Other;  
 Query Match 75.5%; Score 822; DB 10; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 GCCTCCCACTCTTGGAGTATTTAGCAGCCGCTGTGTGCGCGCCGCGCGGAGGCC 60  
 Qy 124 GCCTACATCGCGGTGGAGTACGTAGACGACACGCAATTCCTGGGGTTGACAGCGACGCC 183

Db 61 CGCTACATCGCGTGGAGTACGTAGACGACACGCAATTCCTGCGTTCGACAGCGAGCC 120  
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 Db 121 GCGATTCGAGATGAGCCCGGAGCGCTGGTGGAGCGAAGAGGGCGCGATTTGG 180  
 Qy 244 GAGTGACACACAGGGGTACGCCAAGGCCAAACGACAGAGTACCGAGTGGCCCTGAGGAAC 303  
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 Qy 364 TGGACATCGGCGCCGACGAGCGGCTCTCCGCGGGTATCACACGACGCGGTACGAGCC 423  
 Db 301 TGGACATCGGCGCCGACGAGCGGCTCTCCGCGGGTATCACACGACGCGGTACGAGCC 360  
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 Qy 484 CAGATCACCCAGCGCTTCTATGAGCGAGGAATATGACAGAGGAGTTTCAGGACCTACCTG 543  
 Db 421 CAGATCACCCAGCGCTTCTATGAGCGAGGAATATGACAGAGGAGTTTCAGGACCTACCTG 480  
 Qy 544 GAGGCGAGTGGCTGGAGTTGCTCCGAGATACTTGGAGATGGAGAGAGAGCGTACAG 603  
 Db 481 GAGGCGAGTGGCTGGAGTTGCTCCGAGATACTTGGAGATGGAGAGAGAGCGTACAG 540  
 Qy 604 CGCGCAGATCTCCAAAGGCGACACGTTGCCACACACCCCATCTCTGACCATGAGGCCACC 663  
 Db 541 CGCGCAGATCTCCAAAGGCGACACGTTGCCACACACCCCATCTCTGACCATGAGGCCACC 600  
 Qy 664 CTGAGTGTCTGGCGCTGGGCTTACCTCGGAGATCAGCTGACCTGGAGCGGAT 723  
 Db 601 CTGAGTGTCTGGCGCTGGGCTTACCTCGGAGATCAGCTGACCTGGAGCGGAT 660  
 Qy 724 GGGGAGAAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTCGAGGGGATGGAAC 783  
 Db 661 GGGGAGAAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTCGAGGGGATGGAAC 720  
 Qy 784 TTCCAGAGTGGCGCTGTGTGTGCTTCTGGAGAGGACAGAGATACATGCCAT 843  
 Db 721 TTCCAGAGTGGCGCTGTGTGTGCTTCTGGAGAGGACAGAGATACATGCCAT 780  
 Qy 844 GTGAGCAGAGGGGCTGCCCGCCCTCATCTCTGAGATGG 885  
 Db 781 GTGAGCAGAGGGGCTGCCCGCCCTCATCTCTGAGATGG 822

RESULT 11  
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 ID AAC78195 standard; cDNA; 816 BP.  
 XX  
 AC AAC78195;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human cancer associated gene sequence SEQ ID NO:589.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulvar; immunomodulator;  
 KW anti-infective; antitubercular; antirheumatic; antidiabetic; antiviral;  
 KW anti-inflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nontropic;  
 KW vasorelaxant; antiproliferative; angiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening; ss.  
 XX

OS Homo sapiens.  
 XX W020005350-A1.  
 XX PD 21-SEP-2000.  
 XX 08-MAR-2000; 2000WO-US005882.  
 XX PR 12-MAR-1999; 99US-0124270P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Ruben SM;  
 XX DR WPI; 2000-587533/55.  
 XX DR P-PSDB; AAB43986.  
 XX Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.  
 XX PS Claim 1; Page 1111-1112; 2352pp; English.  
 XX CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB4398 to AAB4439. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnerary; immunomodulator;  
 CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX SQ Sequence 816 BP; 165 A; 258 C; 268 G; 125 T; 0 U; 0 Other;  
 Query Match 72.2%; Score 786; DB 3; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGCGCGCCGGAAGCCTCTCTGCTGCTCTCAGGGGCGCTGGCCCTGACCGATCTTGG 60  
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 QY 61 GCGGGCTCCACCTCTTGGAGTATTTACACCGCTGTGCGCGCGCGCGCGGGGAG 120  
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 DB 200 GCGCGATTCGAGGATGAGCGCGGGAGCGGTGGAGCAAGAGGGCGCGCAGTAT 259  
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 QY 301 AACCTGCTCCGCGCTACAAACACAGAGCGAGGCTGGTCTCACACCTCCAGGGAATGAAT 360  
 DB 320 AACCTGCTCCGCGCTACAAACACAGAGCGAGGCTGGTCTCACACCTCCAGGGAATGAAT 379

QY 361 GGCTGCACATGGGGCCGAGCGCTCTCTCGCGGGTATCACAGACCGGTACGAC 420  
 DB 380 GGCTGCACATGGGGCCGAGCGCTCTCTCGCGGGTATCACAGACCGGTACGAC 439  
 QY 421 GGCAGGATTACATCTCCCTGAACAGGACCTGCGCTCTCTGACCGCGCGGACACCGTG 480  
 DB 440 GGCAGGATTACATCTCCCTGAACAGGACCTGCGCTCTCTGACCGCGCGGACACCGTG 499  
 QY 481 GCTCAGATCAACCCAGCGCTTCTATGAGGCGAGAGAAATATGAGAGAGTTTACGAGCCTAC 540  
 DB 500 GCTCAGATCAACCCAGCGCTTCTATGAGGCGAGAGAAATATGAGAGAGTTTACGAGCCTAC 559  
 QY 541 CTGAGGGCGAGTCCCTGGAGTTCTCCGAGATCTTGGAGATGGAGAGGAGAGCGCTA 600  
 DB 560 CTGAGGGCGAGTCCCTGGAGTTCTCCGAGATCTTGGAGATGGAGAGGAGAGCGCTA 619  
 QY 601 CAGCGCGCAGATCCTCCAAAGGCACAGTTTGGCCACCCACCCCATCTCTGACCATGAGGCC 660  
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 QY 661 ACCCTGAGGTGCTGGGCGCTTCTACCTGCGGAGATCAGCTGACCTGGCGAGCGG 720  
 DB 680 ACCCTGAGGTGCTGGGCGCTTCTACCTGCGGAGATCAGCTGACCTGGCGAGCGG 739  
 QY 721 GATGGGAGGAAACAGACCCAGGACACAGAGCTTGTGGAGACCGGCTCGAGGGATGGA 780  
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 DB 800 ACCTTC 805  
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 ID AAH45557 standard; DNA; 645 BP.  
 XX AC AAH45557;  
 XX DT 12-SEP-2001 (first entry)  
 XX DE Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 3.  
 XX KW HLA-F antigen; cancer cell specific; human; ds.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
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 FT /\*tag= a  
 FT /partial  
 FT /product= "Cancer cell specific HLA-F antigen"  
 XX JP2001095584-A.  
 XX PD 10-APR-2001.  
 XX PF 30-SEP-1999; 99JP-00279566.  
 XX PR 30-SEP-1999; 99JP-00279566.  
 XX PA (EGAW/) EGAWA K.  
 XX PA (MEDI-) MEDINET KK.  
 XX PA (KIMU/) KIMURA K.  
 XX WIPI; 2001-360493/38.  
 XX DR P-PSDB; AAG64619.  
 XX PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
 XX PS Claim 3; Page 9; 12pp; Japanese.  
 XX

CC This invention relates to a cancer cell specific HLA-F antigen. The  
 CC invention includes DNA encoding the antigen, and a method for the  
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
 CC used in a method to diagnose cancer, in which the protein is used to  
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
 CC sequence represents DNA encoding the cancer cell-specific HLA-F antigen  
 CC of the invention  
 XX

SQ Sequence 645 BP; 143 A; 194 C; 215 G; 93 T; 0 U; 0 Other;

Query Match 59.2%; Score 645; DB 4; Length 645;

Best Local Similarity 100.0%; Pred. No. 9e-296;

Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ATCCGCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTCCGACGCGACCGCGGATT 189  
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 QY 190 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGAGCAAGAGGGCCCGCAGTATTGGAGTGG 249  
 DB 61 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGAGCAAGAGGGCCCGCAGTATTGGAGTGG 120  
 QY 250 ACCCAGGATACGCGCAGGCGCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 309  
 DB 121 ACCCAGGATACGCGCAGGCGCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 180  
 QY 310 CGCGCTACACAGCGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 369  
 DB 181 CGCGCTACACAGCGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 240  
 QY 370 ATGGGGCCCGCAGGAGCCTCTCCGCGGTATCCACGACGCGCTACGACGCGCAAGGAT 429  
 DB 241 ATGGGGCCCGCAGGAGCCTCTCCGCGGTATCCACGACGCGCTACGACGCGCAAGGAT 300  
 QY 430 TACATCTCCCTGAACGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 489  
 DB 301 TACATCTCCCTGAACGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 360  
 QY 490 ACCCAGGCTTCTATGAGGAGAGGATATGACAGGAGTTCAGGACCTACCTGGAGGCG 549  
 DB 361 ACCCAGGCTTCTATGAGGAGAGGATATGACAGGAGTTCAGGACCTACCTGGAGGCG 420  
 QY 550 GAGTCCCTGGAGTGGTCTCCGAGATATCTGGAGATGGGAAGAGACGCTACAGCGCGCA 609  
 DB 421 GAGTCCCTGGAGTGGTCTCCGAGATATCTGGAGATGGGAAGAGACGCTACAGCGCGCA 480  
 QY 610 GATCTCTCAAGGACACAGCTTGGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 669  
 DB 481 GATCTCTCAAGGACACAGCTTGGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540  
 QY 670 TGTGGGCGCTGGGCTTACCTCTGGGAGATACGCTGACCTGGGAGCGGATGGGAG 729  
 DB 541 TGTGGGCGCTGGGCTTACCTCTGGGAGATACGCTGACCTGGGAGCGGATGGGAG 600  
 QY 730 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGACGGG 774  
 DB 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACGAGGCTGACGGG 645

RESULT 13

ADP55586

ID ADP55586 standard; DNA; 645 BP.

XX AC

ADP55586;

XX DT

12-FEB-2004 (first entry)

XX DE

DNA encoding fragment #2 of human cancer-cell specific HLA-F antigen.

XX KW

Cancer; human leukocyte antigen-F; HLA-F;

XX KW

cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;

XX KW

major histocompatibility complex; MHC; cancer cell; human; gene; ds.

XX

OS Homo sapiens.  
 XX Key  
 FF Location/Qualifiers  
 CDS 1..645  
 FT /\*tag= a  
 FT /partial  
 FT /note="This sequence lacks both start and stop codons"  
 XX  
 PN JP2003012544-A.  
 XX 15-JAN-2003.  
 XX 27-MAR-2002; 2002JP-00088991.  
 XX 27-MAR-2001; 2001JP-00090121.  
 XX (EGAW/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (XIMU/) KIMURA Y.  
 XX WPI; 2003-486263/46.  
 DR P-PSDB; ADF55589.  
 XX Agent for preventing and treating cancer, comprising human leukocyte  
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
 XX Disclosure; SEQ ID NO 3; 19pp; Japanese.  
 XX The present invention relates to an agent for preventing or treating  
 CC cancer. The agent comprises a portion or a complete sequence of a human  
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
 CC unrestricted to the major histocompatibility complex (MHC) and specific  
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
 CC is useful for treating or preventing cancer. A cell capable of presenting  
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
 CC for diagnosing cancer. The present sequence encodes part of the human  
 CC cancer-cell specific HLA-F antigen.  
 XX  
 SQ Sequence 645 BP; 143 A; 194 C; 215 G; 93 T; 0 U; 0 Other;

Query Match 59.2%; Score 645; DB 10; Length 645;

Best Local Similarity 100.0%; Pred. No. 9e-296;

Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ATCCGCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTCCGACGCGACCGCGGATT 189  
 DB 1 ATCCGCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTCCGACGCGACCGCGGATT 60  
 QY 190 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGAGCAAGAGGGCCCGCAGTATTGGAGTGG 249  
 DB 61 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGAGCAAGAGGGCCCGCAGTATTGGAGTGG 120  
 QY 250 ACCCAGGATACGCGCAGGCGCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 309  
 DB 121 ACCCAGGATACGCGCAGGCGCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 180  
 QY 310 CGCGCTACACAGCGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 369  
 DB 181 CGCGCTACACAGCGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 240  
 QY 370 ATGGGGCCCGCAGGAGCCTCTCCGCGGTATCCACGACGCGCTACGACGCGCAAGGAT 429  
 DB 241 ATGGGGCCCGCAGGAGCCTCTCCGCGGTATCCACGACGCGCTACGACGCGCAAGGAT 300  
 QY 430 TACATCTCCCTGAACGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 489  
 DB 301 TACATCTCCCTGAACGAGGAGTGGTCTCACACCTCCAGGCAATGAATGGCTCGAC 360  
 QY 490 ACCCAGGCTTCTATGAGGAGAGGAAATGACAGGAGTTCAGGACCTACCTGGAGGCG 549



CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
 CC determined by the technique of SBH (sequencing by hybridisation). Also  
 CC included is a purified polypeptide comprising a sequence corresponding to  
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
 CC are useful in diagnostics as expressed sequence tags (EST) for  
 CC identifying expressed genes or for physical mapping of the human genome,  
 CC in forensics, in assessing biodiversity, or in identifying mutations  
 CC responsible for genetic disorders and other traits. The nucleotide  
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
 CC for chromosome and gene mapping, in the recombinant production of  
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
 CC is useful for generating antibodies specific for it. The present sequence  
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
 XX  
 SQ Sequence 487 BP; 97 A; 154 C; 159 G; 73 T; 0 U; 4 Other;

Query Match 32.6%; Score 355; DB 9; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-158;  
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	144	CGTAGACACACGCAATTCCTGGGTTCCGAGCAGCGCGGATTCGAGGATGGAGCC	203
DB	132	CGTAGACACACGCAATTCCTGGGTTCCGAGCAGCGCGGATTCGAGGATGGAGCC	191
QY	204	CGGGAGCCGTGGGTGGAGCAAGAGGGGCGCAGTATGGGAGTGGACACAGGGTACGC	263
DB	192	CGGGAGCCGTGGGTGGAGCAAGAGGGGCGCAGTATGGGAGTGGACACAGGGTACGC	251
QY	264	CAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTCCGCCGCTACAAACA	323
DB	252	CAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTCCGCCGCTACAAACA	311
QY	324	GAGCGAGCCTGGTCTCACACCTCCAGGGAATGATGGCTCGGACATGGGCGCGAGCG	383
DB	312	GAGCGAGCCTGGTCTCACACCTCCAGGGAATGATGGCTCGGACATGGGCGCGAGCG	371
QY	384	ACGCCCTCCTCCGCCGGTATCACCAGCACGGGTACGACGGCAAGGATTACATCTCCCTGAA	443
DB	372	ACGCCCTCCTCCGCCGGTATCACCAGCACGGGTACGACGGCAAGGATTACATCTCCCTGAA	431
QY	444	CGAGGACCTGGCTCCTGGACCGCGCGGACACGGTGGCTCAGATCACCACGCGC	498
DB	432	CGAGGACCTGGCTCCTGGACCGCGCGGACACGGTGGCTCAGATCACCACGCGC	486

Search completed: December 16, 2004, 13:07:23  
 Job time : 637 secs



QY 241 TGGAGTGGACACACAGGTAGCGCAAGCCCAAGCCACAGACTGACCGAGTGGCCCTTGAGG 300  
DB 304 TGGAGTGGACACACAGGTAGCGCAAGCCCAAGCCCAAGCCACAGACTGACCGAGTGGCCCTTGAGG 363  
QY 301 AACCTGCTCCGCGCTCAACACAGAGCGAGGCTGGGTCTCACACCCCTCCAGGGAATGAAT 360  
DB 364 AACCTGCTCCGCGCTCAACACAGAGCGAGGCTGGGTCTCACACCCCTCCAGGGAATGAAT 423  
QY 361 G 361  
DB 424 G 424

## RESULT 2

US-09-799-451-322  
; Sequence 322, Application US/09799451  
; Patent No. 6783969

## GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyang  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt\_FL\_Genes Version 2.0  
; SEQ ID NO 322  
; LENGTH: 1221  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(213)

US-09-799-451-322

Query Match 6.7%; Score 73; DB 4; Length 1221;

Best Local Similarity 100.0%; Pred. No. 5.4e-25;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 691  
DB 769 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 828

QY 692 CTGCGGAGATCAC 704

DB 829 CTGCGGAGATCAC 841

## RESULT 3

US-09-566-921-130

; Sequence 130, Application US/09566921

; Patent No. 6682888

## GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.  
; APPLICANT: Tingley, Debora W.

; APPLICANT: Edwards, Carla M.  
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE  
; FILE REFERENCE: PA-0024 US  
; CURRENT APPLICATION NUMBER: US/09/566,921  
; CURRENT FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: PERL Program  
; SEQ ID NO 130  
; LENGTH: 1521  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6682888 1040429.6

US-09-566-921-130

## Query Match

6.7%; Score 73; DB 4; Length 1521;

Best Local Similarity 100.0%; Pred. No. 5.3e-25;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 691  
DB 645 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 704

QY 692 CTGCGGAGATCAC 704

DB 705 CTGCGGAGATCAC 717

## RESULT 4

US-09-799-451-317

; Sequence 317, Application US/09799451

; Patent No. 6783969

## GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyang  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt\_FL\_Genes Version 2.0  
; SEQ ID NO 317  
; LENGTH: 1559  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (43)..(681)

US-09-799-451-317

## Query Match

6.7%; Score 73; DB 4; Length 1559;

Best Local Similarity 100.0%; Pred. No. 5.3e-25;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 691

```
Db 685 CCACACCCCATCTCTGACCATGAGGCCACCATCTGAGTGTGGGCGCTTCTTACC 744
QY 692 CTGCGGAGATCAC 704
Db 745 CTGCGGAGATCAC 757

RESULT 5
US-08-522-942-1
; Sequence 1, Application US/08522942
; Patent No. 5753442
; GENERAL INFORMATION:
; APPLICANT: Tyan, Dolly B.
; TITLE OF INVENTION: METHOD FOR DETERMINING GENETIC
; TITLE OF INVENTION: PREPOSITION FOR SERONEGATIVE SPONDYLOARTHRITIS AND
; TITLE OF INVENTION: PRODUCTS THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4365 Executive Drive, Suite 1500
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/522,942
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P07 33624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-1995
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-522-942-1

Query Match 6.7%; Score 73; DB 1; Length 653;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCACACCCCATCTCTGACCATGAGGCCACCATCTGAGTGTGGGCGCTTCTTACC 691
Db 2269 CCACACCCCATCTCTGACCATGAGGCCACCATCTGAGTGTGGGCGCTTCTTACC 2328

QY 692 CTGCGGAGATCAC 704
Db 2329 CTGCGGAGATCAC 2341

RESULT 6
US-09-513-999C-12022
; Sequence 12022, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
```

```
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 12022
; LENGTH: 152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-12022

Query Match 6.0%; Score 65; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCGCCCGAAGCCTCTCTGCTCTCTGCTCTCTGAGGCGCCCTGCGCTTCTTGG 60
Db 64 ATGGGCGCCCGAAGCCTCTCTGCTCTCTGCTCTCTGAGGCGCCCTGCGCTTCTTGG 123
QY 61 GCGGG 65
Db 124 GCGGG 128

RESULT 7
US-09-799-451-318/c
; Sequence 318, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Resna
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_FL_genes Version 2.0
; SEQ ID NO 318
; LENGTH: 2225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1140)..(1769)
US-09-799-451-318

Query Match 5.6%; Score 61; DB 4; Length 2225;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 TCTCTGACCATGAGGCCACCATCTGAGTGTGGGCGCTTCTTACCCTTGGGAGATCA 703
Db 449 TCTCTGACCATGAGGCCACCATCTGAGTGTGGGCGCTTCTTACCCTTGGGAGATCA 390
```

```
QY 704 C 704
Db 389 C 389

RESULT 8
US-09-220-132-84
; Sequence 84, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 3520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-84

Query Match 5.6%; Score 61; DB 4; Length 3520;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 TCTGTGACCATGAGGCGCCACCTGAGTGTGGGCGGCTTCTACCTGCGGAGATCA 703
Db 1690 TCTGTGACCATGAGGCGCCACCTGAGTGTGGGCGGCTTCTACCTGCGGAGATCA 1749

QY 704 C 704
Db 1750 C 1750

RESULT 9
US-09-799-451-318
; Sequence 318, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunzui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 318
; LENGTH: 2225
```

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1140)...(1769)
US-09-799-451-318

Query Match 4.8%; Score 52; DB 4; Length 2225;
Best Local Similarity 100.0%; Pred. No. 4.6e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCGCCACCTGAGTGTGGGCGGCTGGG 683
Db 1773 CCCACACCCCATCTCTGACCATGAGGCGCCACCTGAGTGTGGGCGGCTGGG 1824

RESULT 10
US-08-564-313-2/c
; Sequence 2, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92860
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7
US-08-564-313-2

Query Match 4.8%; Score 52; DB 2; Length 4059;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCGCCACCTGAGTGTGGGCGGCTGGG 683
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Db 2243 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 2192

## RESULT 11

PCT-US94-06069-2/c  
; Sequence 2, Application PC/TUS9406069  
; GENERAL INFORMATION:  
; APPLICANT: Vical Incorporated  
; APPLICANT: Regents of the University of Michigan  
; APPLICANT: Nabel, Elizabeth  
; APPLICANT: Nabel, Gary  
; APPLICANT: Lew, Denise  
; APPLICANT: Marquet, Magda  
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/06069  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/074,344  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: VICAL 033VPC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4059 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; STRAIN: HLA-B7  
; PCT-US94-06069-2

Query Match 4.8%; Score 52; DB 5; Length 4059;  
Best Local Similarity 100.0%; Pred. No. 4.5e-15;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 683  
Db 2243 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 2192

## RESULT 12

US-08-564-313-1  
; Sequence 1, Application US/08564313  
; Patent No. 5910488  
; GENERAL INFORMATION:  
; APPLICANT: Nabel, Elizabeth  
; APPLICANT: Nabel, Gary

; APPLICANT: Lew, Denise  
; APPLICANT: Marquet, Magda  
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/564,313  
; FILING DATE: 01-DEC-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/074,344  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: VICAL 033CPI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4965 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; IMMEDIATE SOURCE:  
; CLONE: HLA-B7 and Beta-2  
; US-08-564-313-1

Query Match 4.8%; Score 52; DB 2; Length 4965;  
Best Local Similarity 100.0%; Pred. No. 4.5e-15;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 683  
Db 1175 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 1226

## RESULT 13

PCT-US94-06069-1  
; Sequence 1, Application PC/TUS9406069  
; GENERAL INFORMATION:  
; APPLICANT: Vical Incorporated  
; APPLICANT: Regents of the University of Michigan  
; APPLICANT: Nabel, Elizabeth  
; APPLICANT: Nabel, Gary  
; APPLICANT: Lew, Denise  
; APPLICANT: Marquet, Magda  
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1

Query Match 4.8%; Score 52; DB 5; Length 4965;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 632 CCCACCCCATCTTGACCATGAGCCACCTTGAGGTGCTGGGCGCTGGG 683
Db 1175 CCCACCCCATCTTGACCATGAGCCACCTTGAGGTGCTGGGCGCTGGG 1226

RESULT 14
US-08-403-853-13
Sequence 13, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: AIWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..363
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
US-08-403-853-13

Query Match 4.6%; Score 50; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 748 GAGCTTGTGGAGACCCAGGCTGCGAGGGATGGAACCTTCCAGAAAGTGGC 797
Db 196 GAGCTTGTGGAGACCCAGGCTGCGAGGGATGGAACCTTCCAGAAAGTGGC 245

RESULT 15
US-09-397-787-329
Sequence 329, Application US/09397787
Patent No. 6468758
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 329
LENGTH: 438
TYPE: DNA
ORGANISM: Homo sapien
US-09-397-787-329

Query Match 4.6%; Score 50; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 748 GAGCTTGTGGAGACCCAGGCTGCGAGGGATGGAACCTTCCAGAAAGTGGC 797
Db 158 GAGCTTGTGGAGACCCAGGCTGCGAGGGATGGAACCTTCCAGAAAGTGGC 207

Search completed: December 16, 2004, 17:03:52
Job time : 122 secs
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QY 181 GCGCGATTCCGAGATGAGCCGCGGAGCCGCTGGTGGAGCAAGAGGGGCGCAGTAT 240
DB 181 GCGCGATTCCGAGATGAGCCGCGGAGCCGCTGGTGGAGCAAGAGGGGCGCAGTAT 240
QY 241 TGGGAGTGGACACACAGGGGTAGCCCAAGCCAAACGACAGACTGACCGAGTGGCCCTGAGG 300
DB 241 TGGGAGTGGACACACAGGGGTAGCCCAAGCCAAACGACAGACTGACCGAGTGGCCCTGAGG 300
QY 301 AACCTGCTCCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360
DB 301 AACCTGCTCCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360
QY 361 GGTCTCGCATGGGGCCCGCGGACGCTCTCCGCGGGTATCACACGACGCGTACGAC 420
DB 361 GGTCTCGCATGGGGCCCGCGGACGCTCTCCGCGGGTATCACACGACGCGTACGAC 420
QY 421 GCGAGGATTACATCTCCCTGAAACGAGGACTCGCTCTGGACCGCGGAGACCGG 480
DB 421 GCGAGGATTACATCTCCCTGAAACGAGGACTCGCTCTGGACCGCGGAGACCGG 480
QY 481 GGTCTCGCATGGGGCCCGCGGACGCTCTCCGCGGGTATCACACGACGCGTACGAC 540
DB 481 GGTCTCGCATGGGGCCCGCGGACGCTCTCCGCGGGTATCACACGACGCGTACGAC 540
QY 541 CTGAGGCGGAGTGGCTGGAGTTCCTCGGAGATACCTGAGGAGTGGAGAGGAGCGTA 600
DB 541 CTGAGGCGGAGTGGCTGGAGTTCCTCGGAGATACCTGAGGAGTGGAGAGGAGCGTA 600
QY 601 CAGCGCGGAGATCTCCAAAGGACACAGTTCGCCACCAACCCCATCTCTGACATGAGGC 660
DB 601 CAGCGCGGAGATCTCCAAAGGACACAGTTCGCCACCAACCCCATCTCTGACATGAGGC 660
QY 661 ACCCTGAGGTGCTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGAGCGG 720
DB 661 ACCCTGAGGTGCTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGAGCGG 720
QY 721 GATGGGAGGAAACAGACCCAGGACACAGAGTTCGAGAGCCAGGCTCGAGGGATGA 780
DB 721 GATGGGAGGAAACAGACCCAGGACACAGAGTTCGAGAGCCAGGCTCGAGGGATGA 780
QY 781 ACCTTCAGAGTGGGCGCTGCTGGTGGCTTCTGAGAGGAAACAGAGATACATGC 840
DB 781 ACCTTCAGAGTGGGCGCTGCTGGTGGCTTCTGAGAGGAAACAGAGATACATGC 840
QY 841 CATGTGAGCAGAGGGGCTGCCAGCCCTCATCTGAGATGGAGAGTCTCCCGAG 900
DB 841 CATGTGAGCAGAGGGGCTGCCAGCCCTCATCTGAGATGGAGAGTCTCCCGAG 900
QY 901 CCCACCATCCCATCGTGGGCTGCTGGTGGCTTCTGAGAGTGGGTCAC 960
DB 901 CCCACCATCCCATCGTGGGCTGCTGGTGGCTTCTGAGAGTGGGTCAC 960
QY 961 GGAGCTGTGCTGCTGCTGATGTGAGAGGAAAGAGCTCAGATGAACAGAGGAGC 1020
DB 961 GGAGCTGTGCTGCTGCTGATGTGAGAGGAAAGAGCTCAGATGAACAGAGGAGC 1020
QY 1021 TACTCTCAGGCTGAGTCACTGACAGTGGCCAGGCTCTGGGTGCTCTCAGAGTAAT 1080
DB 1021 TACTCTCAGGCTGAGTCACTGACAGTGGCCAGGCTCTGGGTGCTCTCAGAGTAAT 1080
QY 1081 AAAGTGTA 1089
DB 1081 AAAGTGTA 1089

```

## RESULT 2

US-10-172-118-1806

; Sequence 1806, Application US/10172118  
; Publication No. US20030224374A1

## GENERAL INFORMATION:

; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter

```

; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1806
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_018950
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-1806

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Query Match 100.0%; Score 1089; DB 15; Length 1188;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCGCCCGGAGCCTCTCTGCTCTCAGGGCCCTGGCCCTGACCGCATCTGG 60
DB 1 ATGCGCCCGGAGCCTCTCTGCTCTCAGGGCCCTGGCCCTGACCGCATCTGG 60
QY 61 GCGGGTCCCACTCTCTGAGTATTTACGACACCGCTGTCTCGGCGCCGCGCGGAG 120
DB 61 GCGGGTCCCACTCTCTGAGTATTTACGACACCGCTGTCTCGGCGCCGCGCGGAG 120
QY 121 CCCCGTACATCGCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTCCGACGCGAC 180
DB 121 CCCCGTACATCGCGTGGAGTACGTAGACGACACGCAATTCCTCGGTTCCGACGCGAC 180
QY 181 GCGCGCATCCGAGATGGAGCCGCGGAGCGGTGGTGGAGCAAGAGGGGCGCAGTAT 240
DB 181 GCGCGCATCCGAGATGGAGCCGCGGAGCGGTGGTGGAGCAAGAGGGGCGCAGTAT 240
QY 241 TGGGAGTGGACACACAGGGGTACGCCAAGCCAAACGACAGACTGACCGAGTGGCCCTGAGG 300
DB 241 TGGGAGTGGACACACAGGGGTACGCCAAGCCAAACGACAGACTGACCGAGTGGCCCTGAGG 300
QY 301 AACCTGCTCCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360
DB 301 AACCTGCTCCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360
QY 361 GGTCTGAGCATGGGGCCCGAGCGGCTCTCTCGGCGGTATCACAGCAGCGCTACGAC 420
DB 361 GGTCTGAGCATGGGGCCCGAGCGGCTCTCTCGGCGGTATCACAGCAGCGCTACGAC 420
QY 421 GGCAAGGATACATCTCTCTGAAACGAGGACTGCGCTCTCTGGAACCGCGGAGCACCGTG 480
DB 421 GGCAAGGATACATCTCTCTGAAACGAGGACTGCGCTCTCTGGAACCGCGGAGCACCGTG 480
QY 481 GCTCAGATCACCCAGCGCTTCTATGAGGACAGAGGAATATGAGAGGAGTTCCAGGACCTAC 540
DB 481 GCTCAGATCACCCAGCGCTTCTATGAGGACAGAGGAATATGAGAGGAGTTCCAGGACCTAC 540
QY 541 CTGAGGCGGAGTGGCTGGAGTTCCTCGGAGATACCTGAGAGATGGAGAGGAGACGCTA 600
DB 541 CTGAGGCGGAGTGGCTGGAGTTCCTCGGAGATACCTGAGAGATGGAGAGGAGACGCTA 600
QY 601 CAGCGCGGAGATCTCCAAAGGACACAGTTCGCCACCAACCCCATCTCTGACATGAGGC 660
DB 601 CAGCGCGGAGATCTCCAAAGGACACAGTTCGCCACCAACCCCATCTCTGACATGAGGC 660
QY 661 ACCCTGAGGTGCTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGAGCGG 720
DB 661 ACCCTGAGGTGCTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGAGCGG 720

```





Db 754 GGAGAGAAACAGAGATACATGCCATGTGCAGACGAGGGGTGCCCCAGCCCTCATC 813  
 Qy 877 CTGAGATGG 885  
 Db 814 CTGAGATGG 822

RESULT 6

US-09-819-371-3  
 ; Sequence 3, Application US/09819371  
 ; Publication No. US20040053344A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FROM VARIOUS CDNA LIBRARIES  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; CURRENT FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 645  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-819-371-3

Query Match 45.3%; Score 493; DB 11; Length 645;  
 Best Local Similarity 99.7%; Pred. No. 3.3e-246;  
 Matches 593; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 180 CGCCGGGATTCAGAGATGGAGCGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTA 239  
 Db 51 CGCCGGGATTCAGAGATGGAGCGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTA 110  
 Qy 240 TTGGAGTGGACACAGAGTACGCCAGGCCAACCCACAGACTGACCGAGTGGCCCTGAG 299  
 Db 111 TTGGAGTGGACACAGAGTACGCCAGGCCAACCCACAGACTGACCGAGTGGCCCTGAG 170  
 Qy 300 GAACCTGCTCCGCGGTACAAACAGAGGAGGCTGGGTCTCACACCTCTCCAGGGAATGAA 359  
 Db 171 GAACCTGCTCCGCGGTACAAACAGAGGAGGCTGGGTCTCACACCTCTCCAGGGAATGAA 230  
 Qy 360 TGCGTGGACATGGGGCCCGAGCGAGCTCTCCGCGGTATACAGACGCGTACGA 419  
 Db 231 TGCGTGGACATGGGGCCCGAGCGAGCTCTCCGCGGTATACAGACGCGTACGA 290  
 Qy 420 CGCAAGGATTAATCTCCCTGAAACGAGGACCTGCGCTCTCGGACCGCGGACACCGT 479  
 Db 291 CGCAAGGATTAATCTCCCTGAAACGAGGACCTGCGCTCTCGGACCGCGGACACCGT 350  
 Qy 480 GGCTCAGATACCCAGCGCTTCTATGAGCAGAGGAATATGACAGAGGTTTCAGACCTA 539  
 Db 351 GGCTCAGATACCCAGCGCTTCTATGAGCAGAGGAATATGACAGAGGTTTCAGACCTA 410  
 Qy 540 CTTGGAGGGAGTGGCTGAGTTGCTCCGAGATACCTTGGAGAAATGGAGAGAGCGCT 599  
 Db 411 CTTGGAGGGAGTGGCTGAGTTGCTCCGAGATACCTTGGAGAAATGGAGAGAGCGCT 470  
 Qy 600 ACAGCGCGAGATCTCCAAAGACACAGTTGCCACACCCATCTCTGACCATGAGGC 659  
 Db 471 ACAGCGCGAGATCTCCAAAGACACAGTTGCCACACCCATCTCTGACCATGAGGC 530  
 Qy 660 CACCTGAGTGTGGGGCTGGGCTTCTACCTCGGAGATACGCTGACCTGGCAGCG 719  
 Db 531 CACCTGAGTGTGGGGCTGGGCTTCTACCTCGGAGATACGCTGACCTGGCAGCG 590  
 Qy 720 GGATGGGAGGACACAGACCCAGACACAGAGCTTGTGGAGACCGGCTGACGGG 774  
 Db 591 GGATGGGAGGACACAGACCCAGACACAGAGCTTGTGGAGACCGGCTGACGGG 645

RESULT 7

US-09-918-995-37854

; Sequence 37854, Application US/09918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FROM VARIOUS CDNA LIBRARIES  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; CURRENT FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 37854  
 ; LENGTH: 487  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(487)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-918-995-37854

Query Match 32.6%; Score 355; DB 10; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-174;  
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 144 CGTAGACACACGCAATCTCGGTTCGACAGCGACGCGGATTCGAGGATGGAGCC 203  
 Db 132 CGTAGACACACGCAATCTCGGTTCGACAGCGACGCGGATTCGAGGATGGAGCC 191  
 Qy 204 CGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGACACAGGGGTACGC 263  
 Db 192 CGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTATGGGAGTGACACAGGGGTACGC 251  
 Qy 264 CAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACTGCTCCGCGGTACACCA 323  
 Db 252 CAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACTGCTCCGCGGTACACCA 311  
 Qy 324 GAGCGAGGCTGGGTCTCACACCTCTCCAGGGAATGAATGGCTGCACATGGGGCCGACGG 383  
 Db 312 GAGCGAGGCTGGGTCTCACACCTCTCCAGGGAATGAATGGCTGCACATGGGGCCGACGG 371  
 Qy 384 AGGCTCTCTCGGGGTATACAGACGCGGTACGACGCGGATTAATCTCCCTGAA 443  
 Db 372 AGGCTCTCTCGGGGTATACAGACGCGGTATACAGACGCGGTATTAATCTCCCTGAA 431  
 Qy 444 CGAGGACCTGGCTCTCTCGGACCGCGGACACCGTGGCTCAGATCACCCAGCGC 498  
 Db 432 CGAGGACCTGGCTCTCTCGGACCGCGGACACCGTGGCTCAGATCACCCAGCGC 486

RESULT 8

US-09-880-107-3713  
 ; Sequence 3713, Application US/09880107  
 ; Patent No. US20020142981A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horne, Darci T.  
 ; APPLICANT: Vockley, Joseph G.  
 ; APPLICANT: Scherf, Uwe  
 ; APPLICANT: Gene Logic, Inc.  
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
 ; FILE REFERENCE: 44921-5028-WO  
 ; CURRENT APPLICATION NUMBER: US/09/880,107  
 ; CURRENT FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/211,379  
 ; PRIOR FILING DATE: 2000-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/237,054  
 ; PRIOR FILING DATE: 2000-10-02  
 ; NUMBER OF SEQ ID NOS: 3950  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3713  
 ; LENGTH: 4316

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X17093
US-09-880-107-3713

Query Match      25.6%; Score 279; DB 9; Length 4316;
Best Local Similarity 100.0%; Pred. No. 7.8e-135;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 608 CAGATCTCTCCAAAGGACACAGCTTCCGACACACACCCCATCTCTGACCATGAGGCGACCCCTGA 667
DB 2413 CAGATCTCTCCAAAGGACACAGCTTCCGACACACACCCCATCTCTGACCATGAGGCGACCCCTGA 2472
QY 668 GGTGTGGGGCCCTGGGCTTTACCTCTGGGAGATCAGCTGACCTGGCAGCGGGATGGGG 727
DB 2473 GGTGTGGGGCCCTGGGCTTTACCTCTGGGAGATCAGCTGACCTGGCAGCGGGATGGGG 2532
QY 728 AGGACACAGCCAGGACACAGAGCTTGTGAGACAGGCTGACAGGGATGGAACCTTCC 787
DB 2533 AGGAACACAGCCAGGACACAGAGCTTGTGAGACAGGCTGACAGGGATGGAACCTTCC 2592
QY 788 AGAATGGGGCCGCTGTGTGTGCTTCTCTGGAGAGGACAGATACATGCCATGTGC 847
DB 2593 AGAATGGGGCCGCTGTGTGTGCTTCTCTGGAGAGGACAGATACATGCCATGTGC 2652
QY 848 AGCAGAGGGGCTGCCCCAGCCCTCATCTGTGAGATGGG 886
DB 2653 AGCAGAGGGGCTGCCCCAGCCCTCATCTGTGAGATGGG 2691

RESULT 9
US-10-257-021-81
; Sequence 81, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 4316
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-81

Query Match      25.6%; Score 279; DB 15; Length 4316;
Best Local Similarity 100.0%; Pred. No. 7.8e-135;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 608 CAGATCTCTCCAAAGGACACAGCTTCCGACACACCCCATCTCTGACCATGAGGCGACCCCTGA 667
DB 2413 CAGATCTCTCCAAAGGACACAGCTTCCGACACACCCCATCTCTGACCATGAGGCGACCCCTGA 2472
QY 668 GGTGTGGGGCCCTGGGCTTTACCTCTGGGAGATCAGCTGACCTGGCAGCGGGATGGGG 727
DB 2473 GGTGTGGGGCCCTGGGCTTTACCTCTGGGAGATCAGCTGACCTGGCAGCGGGATGGGG 2532
QY 728 AGGACACAGCCAGGACACAGAGCTTGTGAGACAGGCTGACAGGGATGGAACCTTCC 787
DB 2533 AGGAACACAGCCAGGACACAGAGCTTGTGAGACAGGCTGACAGGGATGGAACCTTCC 2592
QY 788 AGAATGGGGCCGCTGTGTGTGCTTCTCTGGAGAGGACAGATACATGCCATGTGC 847

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DB 2593 AGAATGGGGCCGCTGTGTGTGCTTCTCTGGAGAGGACAGATACATGCCATGTGC 2652
QY 848 AGCAGAGGGGCTGCCCCAGCCCTCATCTGTGAGATGGG 886
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RESULT 10
US-09-764-891-6712
; Sequence 6712, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6712
; LENGTH: 3098
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-6712

Query Match      25.4%; Score 277; DB 10; Length 3098;
Best Local Similarity 100.0%; Pred. No. 9e-134;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 GGTCTCTCACACCCCTCCAGGGAATGAATGGTGGCTGACATGCGGCGCCGACGACGCTCTCTC 393
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QY 394 CGCGGGTATCACACAGCAGCGCTGACGAGGCAAGATTACATCTCCCTGACGAGGACCTG 453
DB 802 CGCGGGTATCACACAGCAGCGCTGACGAGGCAAGATTACATCTCCCTGACGAGGACCTG 861
QY 454 CGCTCTCTGACCGCGCGGCGGACACCGTGGCTGACATCCACGAGCGCTTCTATGAGGACAG 513
DB 862 CGCTCTCTGACCGCGCGGCGGACACCGTGGCTGACATCCACCGAGCGCTTCTATGAGGACAG 921
QY 514 GAATATGACAGAGGAGTTTCAGACCTTCTGAGGCGGAGTGCTGGAGTTGCTCCGACAG 573
DB 922 GAATATGACAGAGGAGTTTCAGACCTTCTGAGGCGGAGTGCTGGAGTTGCTCCGACAG 981
QY 574 TACTTGGAGATGGGAGGACACGCTTACAGCGGCGAG 610
DB 982 TACTTGGAGATGGGAGGAGGACGCTACAGCGGCGAG 1018

RESULT 11
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; Sequence 573, Application US/10091572
; Publication No. US20030054373A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA118C1
; CURRENT APPLICATION NUMBER: US/10/091,572
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,850
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,896
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758

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1	PRIOR FILING DATE: 2000-08-14	2	PRIOR APPLICATION NUMBER: 60/220,963	3	PRIOR FILING DATE: 2000-09-29	4	PRIOR APPLICATION NUMBER: 60/236,367
5	PRIOR FILING DATE: 2000-07-26	6	PRIOR APPLICATION NUMBER: 60/217,496	7	PRIOR FILING DATE: 2000-10-02	8	PRIOR APPLICATION NUMBER: 60/237,039
9	PRIOR FILING DATE: 2000-07-11	10	PRIOR APPLICATION NUMBER: 60/225,447	11	PRIOR FILING DATE: 2000-10-02	12	PRIOR APPLICATION NUMBER: 60/237,038
13	PRIOR FILING DATE: 2000-08-14	14	PRIOR APPLICATION NUMBER: 60/218,290	15	PRIOR FILING DATE: 2000-09-29	16	PRIOR APPLICATION NUMBER: 60/236,370
17	PRIOR FILING DATE: 2000-07-14	18	PRIOR APPLICATION NUMBER: 60/225,757	19	PRIOR FILING DATE: 2000-10-02	20	PRIOR APPLICATION NUMBER: 60/236,802
21	PRIOR FILING DATE: 2000-08-14	22	PRIOR APPLICATION NUMBER: 60/226,868	23	PRIOR FILING DATE: 2000-10-02	24	PRIOR APPLICATION NUMBER: 60/237,037
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33	PRIOR FILING DATE: 2000-08-14	34	PRIOR APPLICATION NUMBER: 60/215,880	35	PRIOR FILING DATE: 2000-10-20	36	PRIOR APPLICATION NUMBER: 60/239,935
37	PRIOR FILING DATE: 2000-07-07	38	PRIOR APPLICATION NUMBER: 60/225,270	39	PRIOR FILING DATE: 2000-10-13	40	PRIOR APPLICATION NUMBER: 60/239,937
41	PRIOR FILING DATE: 2000-08-14	42	PRIOR APPLICATION NUMBER: 60/225,869	43	PRIOR FILING DATE: 2000-10-13	44	PRIOR APPLICATION NUMBER: 60/241,787
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53	PRIOR FILING DATE: 2000-09-21	54	PRIOR APPLICATION NUMBER: 60/234,223	55	PRIOR FILING DATE: 2000-11-08	56	PRIOR APPLICATION NUMBER: 60/249,216
57	PRIOR FILING DATE: 2000-09-21	58	PRIOR APPLICATION NUMBER: 60/228,924	59	PRIOR FILING DATE: 2000-11-17	60	PRIOR APPLICATION NUMBER: 60/249,210
61	PRIOR FILING DATE: 2000-08-30	62	PRIOR APPLICATION NUMBER: 60/224,518	63	PRIOR FILING DATE: 2000-08-22	64	PRIOR APPLICATION NUMBER: 60/226,681
65	PRIOR FILING DATE: 2000-08-14	66	PRIOR APPLICATION NUMBER: 60/236,369	67	PRIOR FILING DATE: 2000-08-14	68	PRIOR APPLICATION NUMBER: 60/225,213
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73	PRIOR FILING DATE: 2000-08-14	74	PRIOR APPLICATION NUMBER: 60/220,964	75	PRIOR FILING DATE: 2000-08-22	76	PRIOR APPLICATION NUMBER: 60/225,214
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93	PRIOR FILING DATE: 2000-10-20	94	PRIOR APPLICATION NUMBER: 60/244,617	95	PRIOR FILING DATE: 2000-08-14	96	PRIOR APPLICATION NUMBER: 60/249,218
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 QY 1017 GAGCTACTCTCAGGCTGCAGT 1037  
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Search completed: December 16, 2004, 17:19:21  
 Job time : 675 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 12:47:28 ; Search time 4075 Seconds  
(without alignments)  
9738.127 Million cell updates/sec

Title: US-09-819-371-1

Perfect score: 1089  
Sequence: 1 atgggccccgaagctctct.....tcacagctataaagtgtga 1089

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3282875 seqs, 18219865908 residues

Word size: 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hlc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	763	70.1	829	6	CD514705
2	757	69.5	926	5	BQ707312
3	703	64.6	897	6	CD512828
4	681	62.5	896	5	BQ588194
5	654	60.1	1130	4	BM917072
6	652	59.9	949	4	BM561951
7	649	59.6	928	5	BQ710481
8	642	59.0	718	4	BG679105
9	635	58.3	875	5	BQ962778
10	630	57.9	931	5	BQ926296
11	614	56.4	892	5	BQ690438
12	613	56.3	790	1	AV752612
13	611	56.1	645	2	BF975616
14	610	56.0	636	2	BF725277
15	609	55.9	612	6	CA391513
16	608	55.8	794	6	CD742827
17	595	54.6	768	4	BG744685
18	586	53.8	666	5	BQ016533
19	585	53.7	709	6	CD365012
20	582	53.4	852	4	BM923524
21	567	52.1	941	5	BQ711754
22	562	51.6	749	4	BG743996
23	551	51.1	705	6	CB529818
24	557	51.1	708	6	CB528498

C	25	555	51.0	805	6	CD368629	UI-H-FT1-
	26	541	49.7	622	4	BM782642	K-EST0043
	27	537	49.3	618	4	BM842679	K-EST0120
C	28	536	49.2	721	6	CD367343	UI-H-FT2-
	29	533	48.9	590	4	BG831090	602786640
	30	529	48.6	933	4	BM456332	AGENCOURT
	31	528	48.5	590	4	BG767374	602741158
C	32	524	48.1	571	2	AW610235	RC2-ST030
	33	524	48.1	699	6	CB529146	UI-H-FT2-
C	34	506	46.5	968	5	BQ709603	AGENCOURT
	35	502	46.1	528	7	CF552976	AGENCOURT
	36	501	46.0	692	6	CA388900	UI-H-FT1-
C	37	494	45.4	684	4	BG757938	602714974
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C	39	473	43.4	699	6	CB528356	UI-H-FT2-
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## ALIGNMENTS

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IMAGE:30408575 5', mRNA sequence.  
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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Blg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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## FEATURES

source  
1. 829  
/organism="Homo sapiens"  
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## ORIGIN

Query Match 70.1%; Score 763; DB 6; Length 829;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db GGGGCTCCACTCTCTGAGTATTCAGACGCTGTCTGCGGGCCGCGGGGAG 132

QY 121 CCGCGTACATCCGCTGAGTACGTAGACGACGCAATCTCTGCGGTTCGACGCGAC 180  
 Db CCGCGTACATCCGCTGAGTACGTAGACGACGCAATCTCTGCGGTTCGACGCGAC 192

QY 181 GCGCGATTCGAGATGAGCCGCGGAGCGGTGGTGAGCAAGAGGGCCGAGTAT 240  
 Db GCGCGATTCGAGATGAGCCGCGGAGCGGTGGTGAGCAAGAGGGCCGAGTAT 252

QY 241 TGGAGTGACACAGGCTACGCAAGCCCAAGCCACAGACTACCGAGTGGCCCTGAGG 300  
 Db TGGAGTGACACAGGCTACGCAAGCCCAAGCCACAGACTACCGAGTGGCCCTGAGG 312

QY 301 AACCTGCTCGCGCTCAACACAGAGCGAGGCTGGTCTCACACCTTCAGAGGAATGAAT 360  
 Db AACCTGCTCGCGCTCAACACAGAGCGAGGCTGGTCTCACACCTTCAGAGGAATGAAT 372

QY 361 GGTCTGCGATGGGCGCCGACGAGCGCTCTCTCGCGGGTATCACAGACGCGTACGAC 420  
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QY 421 GCGAAGGATTACATCTCTGAGGAGCGCTCTGAGGAGCGCGCGGCGGACCGGTG 480  
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RESULT 2  
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 LOCUS  
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 AGENCOURT 8354575 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6281285  
 5' mRNA sequence.

ACCESSION BQ0707312  
 VERSION BQ0707312.1 GI:21846211  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. (bases 1 to 926)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: Dr. Mark Watson  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LUCM2473 row: n column: 06  
 High quality sequence stop: 628.  
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 GGCACGAG(G). Library constructed by Ling Hong in the  
 Laboratory of Gerald M. Rubin (University of California,  
 Berkeley), using 2AP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

ORIGIN

Query Match 69.5%; Score 757; DB 5; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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QY 99 GTGCGGCGCGCGCGCGGAGCGCGCTACATCGCGGTGAGTACGTAGACGACGCA 158  
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QY 159 ATTCTGCGGTTCGACAGCGAGCGCGATTCGAGATGAGCGCGGAGCGCGGTGGT 218  
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QY 219 GAGCAAGAGGGCGCGCGAGTATTTGGAGTGGACACAGGGTACGCCAGGCCAACGACA 278  
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QY 279 GACTGACCGAGTGGCGCTGAGGAACTGTCTCGCGCTACAAACAGAGCGAGGCTGGGTC 338  
 Db GACTGACCGAGTGGCGCTGAGGAACTGTCTCGCGCTACAAACAGAGCGAGGCTGGGTC 337

QY 339 TCACACCTTCGAGGAAATGAATGCTGCGACATGGGCGCGAGCGAGCGCTCTCGCGG 398  
 Db TCACACCTTCGAGGAAATGAATGCTGCGACATGGGCGCGAGCGAGCGCTCTCGCGG 397

QY 399 GTATCACCAGCAGCGGTACGAGCAAGGATTACATCTCCCTGAACGAGGACCTGGGCTC 458  
 Db GTATCACCAGCAGCGGTACGAGCAAGGATTACATCTCCCTGAACGAGGACCTGGGCTC 457

QY 459 CTGGACCGCGGGGACACCGGTGGCTGAGATCACCAGCGCTTTCTATGAGGACAGGAATA 518  
 Db CTGGACCGCGGGGACACCGGTGGCTGAGATCACCAGCGCTTTCTATGAGGACAGGAATA 517

QY 519 TGCAGAGGAGTTTCAAGACCTACCTGGAGGGCGAGTGTCTGAGTTGCTCCGAGATCTT 578  
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QY 579 GAGGATGGAGGAGAGCGCTACAGCGCGAGATCTCTCCAAAGGACACAGCTTCCGCCACA 638  
 Db GAGGATGGAGGAGAGCGCTACAGCGCGAGATCTCTCCAAAGGACACAGCTTCCGCCACA 637

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ACCESSION  
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 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 897)  
 NIH-MGC <http://mgs.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue Procurement: Dr. Michael Brownstein  
 CDNA Library Preparation: Invitrogen Corp  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDAM473 row: 1 column: 01  
 High quality sequence start: 8  
 High quality sequence stop: 707.  
 Location/Qualifiers

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 /organism="Homo sapiens"  
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 /clone="IMAGE:30394728"  
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 /lab\_host="DH10B-Ton A (T1 and T5 phage resistances)"  
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 /notes="Organ: Brain; Vector: pCMV-SPORT6.1; Site: 1: EcoRV  
 (destroyed); Site: 2: NotI; Library is oligo-dr primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.1 kb. Library was  
 constructed by (Invitrogen). Note: this is a NIH\_MGC  
 Library."

FEATURES  
 source  
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 Best Local Similarity 100.0%; Fred. No. 0;  
 Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 GGGTCTCACACCTCCAGGGAATGATGCTCGCATGGGCGCGAGCGGCTCTC 393  
 DB 43 GGGTCTCACACCTCCAGGGAATGATGCTCGCATGGGCGCGAGCGGCTCTC 102  
 QY 394 CGGGGTATCCAGCAGCGGTACGACGCGAGGATTACCTCCCTGACGAGGACTG 453  
 DB 103 CGGGGTATCCAGCAGCGGTACGACGCGAGGATTACCTCCCTGACGAGGACTG 162

ORIGIN  
 Query Match 64.6%; Score 703; DB 6; Length 897;  
 Best Local Similarity 100.0%; Fred. No. 0;  
 Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 GGGTCTCACACCTCCAGGGAATGATGCTCGCATGGGCGCGAGCGGCTCTC 393  
 DB 43 GGGTCTCACACCTCCAGGGAATGATGCTCGCATGGGCGCGAGCGGCTCTC 102  
 QY 394 CGGGGTATCCAGCAGCGGTACGACGCGAGGATTACCTCCCTGACGAGGACTG 453  
 DB 103 CGGGGTATCCAGCAGCGGTACGACGCGAGGATTACCTCCCTGACGAGGACTG 162

QY 454 CGCTCTTGAGCCGCGCGGACACCGTGGCTCAGATCACCCAGCGCTTCTATGAGCAGAG 513  
 DB 163 CGCTCTTGAGCCGCGCGGACACCGTGGCTCAGATCACCCAGCGCTTCTATGAGCAGAG 222  
 QY 514 GAATATGACAGAGAGTTTACGACCTTACCTGGAGGGGAGTGGCTGGAGTTGCTCCGAGA 573  
 DB 223 GAATATGACAGAGAGTTTACGACCTTACCTGGAGGGGAGTGGCTGGAGTTGCTCCGAGA 282  
 QY 574 TACTTGGAGAAATGGGAAGGAGACGCTACAGCGCGCAGATCCTCCAAAGGCACACGTTGCC 633  
 DB 283 TACTTGGAGAAATGGGAAGGAGACGCTACAGCGCGCAGATCCTCCAAAGGCACACGTTGCC 342  
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 QY 694 GCGGAGATCAACGCTGAGCTGGCAGCGGATGGGAGGAAACAGACCCAGACACAGAGCTT 753  
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 QY 754 GTGGAGACCGGCTGAGGAGGATGGAACCTTCCAGAGTGGCGGCTGGTGGTGGCT 813  
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 QY 814 TCTGAGAGGAAACAGAGATACATGCTGATGTCAGCAGAGGGGCTGCCCGAGCCCTC 873  
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 QY 874 ATCTGTAGATGGGAGAGTCTCCCGAGCGGATGGAACCTTCCAGAGTGGCGGCTGGTGGC 933  
 DB 583 ATCTGTAGATGGGAGAGTCTCCCGAGCGGATGGAACCTTCCAGAGTGGCGGCTGGTGGC 642  
 QY 934 CTCTGTGCTCTGGAGCTGTGGTCACTGGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 993  
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 DB 703 AAGAGCTCAGATGAACAGAGGGGAGTCTCTCAGGCTGCAG 745

RESULT 4  
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 DEFINITION AGENCOURT 8064678 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6206180  
 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 EST.  
 BO688194.1 GI:21813510  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 886)  
 NIH-MGC <http://mgs.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LCM2360 row: d column: 21  
 High quality sequence stop: 677.  
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 /db\_xref="taxon:9606"



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QY 481 GCTCAGATCACCCAGCGCTTCTATGAGCAGAGGAATATGACAGAGGAGTTTCAGGACCTAC 540
Db 489 GCTCAGATCACCCAGCGCTTCTATGAGCAGAGGAATATGACAGAGGAGTTTCAGGACCTAC 548
QY 541 CTGAGAGGCGAGTGCTCGAGTTCCTCGCAGATACCTTGGAGATGGAGATGGAGAGGAGCGCTA 600
Db 549 CTGAGAGGCGAGTGCTCGAGTTCCTCGCAGATACCTTGGAGATGGAGATGGAGAGGAGCGCTA 608
QY 601 CAGCGCGGAGATCTCTCCAAAGGACACAGTTCCCAACACCCCATCTCTGACCAT 654
Db 609 CAGCGCGGAGATCTCTCCAAAGGACACAGTTCCCAACACCCCATCTCTGACCAT 662

RESULT 6
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LOCUS BM561951
DEFINITION AGENCOURT_6593172 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5484505
5', mRNA sequence.
ACCESSION BM561951
VERSION BM561951.1 GI:18807627
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2013 row: o column: 02
High quality sequence stop: 682.
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/clone="IMAGE:5484505"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/notes="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 59.9%; Score 652; DB 4; Length 949;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGGCCCGAGAGCTCTCTGCTCTCAGGGGCGCTGCGCTGACCGGATATTGG 60
Db 27 ATGGGGCCCGAGAGCTCTCTGCTCTCAGGGGCGCTGCGCTGACCGGATATTGG 86
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QY 121 CCCCGCTACATCGCCGCTGGAGTACGTAGACGACACACAAATTCCTCGGTTTCACAGCGAC 180
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QY 181 GCGCGGATTCGAGGATGGAGCGCGGGAGCCGCTGGTGGTGGAGCAAGAGGGGCGCGAGTAT 240
Db 207 GCGCGGATTCGAGGATGGAGCGCGGGAGCCGCTGGTGGTGGAGCAAGAGGGGCGCGAGTAT 266
QY 241 TGGAGTGGGACCCACAGGGTACGCCAAAGGCCAACGCAAGCTGACCGAGTGGCGCTGAGG 300
Db 267 TGGAGTGGGACCCACAGGGTACGCCAAAGGCCAACGCAAGCTGACCGAGTGGCGCTGAGG 326
QY 301 AACCTGCTCCGCGCTACAAACACAGAGCGAGGCTGGTCTTCACACCTCCAGGGAATGAAT 360
Db 327 AACCTGCTCCGCGCTACAAACACAGAGCGAGGCTGGTCTTCACACCTCCAGGGAATGAAT 386
QY 361 GCGTGGACATGGGGGCGCGACCGGACGCTCTCCGCGGGGTATCACAGACCGGTACGAC 420
Db 387 GCGTGGACATGGGGGCGCGACCGGACGCTCTCCGCGGGGTATCACAGACCGGTACGAC 446
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QY 481 GCTCAGATCACCCAGCGCTTCTATGAGCAGAGGAATATGACAGAGTTCAGGACCTAC 540
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QY 541 CTGAGGCGGAGTGCCTGGAGTTGCTCCGCGAGATCTTGGAGATGGAGAGGAGCGCTA 600
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QY 661 ACCCTGAGGTGCTGGGCGCTTACCTCCGCGAGATACGCTGACCTGGCAGCGG 720
Db 687 ACCCTGAGGTGCTGGGCGCTTACCTCCGCGAGATACGCTGACCTGGCAGCGG 746
QY 721 GATGGGAGGAAACAGACCCAGGACAGAGCTTG 754
Db 747 GATGGGAGGAAACAGACCCAGGACAGAGCTTG 780

RESULT 7
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LOCUS BM710481
DEFINITION AGENCOURT_8353524 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279516
5', mRNA sequence.
ACCESSION BM710481
VERSION BM710481.1 GI:21849380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: d column: 13
High quality sequence stop: 647.

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QY 422 GCAAGGATTACATCTCCCTGACGAGGACCTGGGCTCCTGGACCGGGCGGACACCGTGG 481

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Db      436  GCAGGATACATCCCTGACGAGGACCTGCGCTCTGACCGCGCGGACACCGTGG 495
Qy      482  CTGAGATCACCAGCGCTTCTATGAGGAGAGGAGATGAGAGAGGTTGAGGACCTACC 541
Db      496  CTGAGATCACCAGCGCTTCTATGAGGAGAGGAGATGAGAGAGGTTGAGGACCTACC 555
Qy      542  TGAGAGGCGAGTGCCTCGGAGTTCCTCGGAGATCTTGGAGATGGAAGAGAGCGCTAC 601
Db      556  TGAGAGGCGAGTGCCTCGGAGTTCCTCGGAGATCTTGGAGATGGAAGAGAGCGCTAC 615
Qy      602  AGCGCGAGATCTCCAAAGGACACGTTGCCACACCCATCTTGCACATGAGGCCA 661
Db      616  AGCGCGAGATCTCCAAAGGACACGTTGCCACACCCATCTTGCACATGAGGCCA 675
Qy      662  CCTGAGGTGCTGGGCGCTTCTACCTTGCAGAGATCA 703
Db      676  CCTGAGGTGCTGGGCGCTTCTACCTTGCAGAGATCA 717

RESULT 9
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LOCUS      875 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8820719 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6380038
5', mRNA sequence.
ACCESSION BO962778
VERSION BO962778.1 GI:22378256
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2567 row: p column: 23
High quality sequence stop: 673.
Location/Qualifiers
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/clone="IMAGE:6380038"
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/clone_lib="NIH_MGC_42"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

ORIGIN
Query Match 58.3%; Score 635; DB 5; Length 875;
Best Local Similarity 99.6%; Pred. No. 5.1e-307;
Matches 785; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      4 ATGGCGCGGAGCTCTCTGCTCTCAGGGCGCTGGCGCTGACCGATCTTGG 63
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Qy      121 CCCGCTACATCGCGCTGGAGTACGTAGACGACACCAATTCCTGCGTTCCAGCGAC 180
Db      124 CCCGCTACATCGCGCTGGAGTACGTAGACGACACCAATTCCTGCGTTCCAGCGAC 183
Qy      181 GCCCGATTCCGAGATGAGCGCGCGGAGCGTGGTGGAGCAAGAGGGCGCGAGTAT 240
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Qy      241 TGGAGTGGACCAACAGGGTACGCCAAGGCCAACCGACAGACTGACCGAGTGCCTGAGG 300
Db      244 TGGAGTGGACCAACAGGGTACGCCAAGGCCAACCGACAGACTGACCGAGTGCCTGAGG 303
Qy      301 AACCTGCTCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCCAGAGGAATGAAT 360
Db      304 AACCTGCTCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCCAGAGGAATGAAT 363
Qy      361 GGCTGGAGATGGGGCGGACGAGCGCTCTCCGCGGGTATCACAGACACGCTACGAC 420
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Qy      421 GGCAAGGATTACATCTCCCTGAACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTG 480
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Qy      601 CAGCGCGAGATCTCCAAAGGACACAGTTGCCACACCGCTCTCTGACCATGAGGCC 660
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Qy      661 ACCCTGAGGTGCTGGGCGCTTCTACCTTCGCGAGATCACGCTGACCTGGCAGCGG 720
Db      664 ACCCTGAGGTGCTGGGCGCTTCTACCTTCGCGAGATCACGCTGACCTGGCAGCGG 723
Qy      721 GATGGAGGAGACAGACCCAGGACAGAGCTTGTGGAGACACCGCTCCAGGGGATGGA 780
Db      724 GATGGAGGAGACAGACCCAGGACAGAGCTTGTGGAGACACCGCTCCAGGGGATGGA 783
Qy      781 ACCTTCCA 788
Db      784 ACCTTCCA 791

RESULT 10
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LOCUS      931 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT_8826885 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6424309
5', mRNA sequence.
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VERSION BO962996.1 GI:22341327
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 931)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov

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Tissue Procurement: DCTD/DTP/Gadgar  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLC2604 row: e column: 14  
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 /note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site: 2:  
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GCCACGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

ORIGIN

Query Match 57.9%; Score 630; DB 5; Length 931;  
 Best Local Similarity 99.9%; Pred. No. 1.6e-304;  
 Matches 680; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 DB 75 GCGGCTCCCACTCTTGGATATTTCAGCACCGCTGTGTGCGGGCCGCGGGGAG 134  
 QY 121 CCCGCTACATCGCGTGGAGTACTAGACGACGCAATTCCTGCGGTTCGACAGCGAC 180  
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 DB 195 GCGGCTCCCACTCTTGGATATTTCAGCACCGCTGTGTGCGGGCCGCGGGGAGTAT 254  
 QY 241 TGGGAGTGACACAGGGTACGCCAAGGCCAAGCAGACGACGAGTGGCCCTGAGG 300  
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 QY 301 AACCTGCTCCGCGCTACACAGCGAGGCTGGGTCTCACCCCTCAGGGAATGAAT 360  
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 QY 541 CTGGAGGCGAGTGGCTGGATCTCTCGGAGATATTGGAGATGGAGGAGACGCTA 600  
 DB 555 CTGGAGGCGAGTGGCTGGATCTCTCGGAGATATTGGAGATGGAGGAGACGCTA 614  
 QY 601 CAGCGCGCAGATCTCTCCAAAGGACACAGCTTGTCCGCCACCCCATCTCTGACCATGAGGCC 660

Db 615 CAGCGCGCAGATCTCTCCAAAGGACACAGCTTGTCCGCCACCCCATCTCTGACCATGAGGCC 674  
 QY 661 ACCCTGAGGTGCTGGGCCCTG 681  
 Db 675 ACCCTGAGGTGCTGGGCCCTG 695  
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 LOCUS AGENCOURT\_8343876 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6248481  
 DEFINITION 5', mRNA sequence.  
 ACCESSION Q6890438  
 VERSION BO690438.1 GI:21815754  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 892)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLC2368 row: g column: 10  
 High quality sequence stop: 623.  
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 /clone="IMAGE:6248481"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;  
 Site: 2: EcoRI; cDNA made by oligo-dt priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GCCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 56.4%; Score 614; DB 5; Length 892;  
 Best Local Similarity 99.8%; Pred. No. 1.8e-296;  
 Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 TGGCGCCCGAGCGCTCTCTGCTCTCAGGGCCCTGGCCCTGACCGTACTTGG 61  
 DB 1 TGGCGCCCGAGCGCTCTCTGCTCTCAGGGCCCTGGCCCTGACCGTACTTGG 60  
 QY 62 CGGGTCCCACTCTTGGATATTTCAGCACCGCTGTGTGCGGGCCGCGGGGAGC 121  
 DB 61 CAGGCTCCCACTCTTGGATATTTCAGCACCGCTGTGTGCGGGCCGCGGGGAGC 120  
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DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLN at:  
 http://image.llnl.gov  
 Plate: L1CM210 row: d column: 19  
 High quality sequence stop: 645.  
 Location/Qualifiers

FEATURES  
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/organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone\_image="4336866"  
 /tissue\_type="primary B-cells from tonsils. (cell line)"  
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 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GCGACGAG(G). Size-selected  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 56.1%; Score 611; DB 2; Length 645;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-295;  
 Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 241 AGTGCTGGGCGCTTCTACCTGCGAGATCACGCTGACCTGGCAGCGGATGGG 300  
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 Db 601 CAGGCTGCAGT 611

RESULT 14

BF725277  
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 DEFINITION

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 636)

Wistow G.J., Bernstein S., Behal A. and Smith D.

NEIBANK: EST analysis and bioinformatics for ocular genomics

Invest. Ophthalmol. Vis. Sci. 41 (2000) In press

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: gracem@helix.nih.gov

Plate: 14 row: a column: 11

Seq primer: M3RPI reverse primer (ABI).

Location/Qualifiers

1..636

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/clone="bx14a11"

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/dev\_stage="Adult"

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/clone\_lib="Human Iris cDNA (Un-normalized, unamplified):  
 EX"

/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris  
 tissue was pooled from 10 individuals ranging in age from  
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 an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A  
 directionally cloned cDNA library in the pCMVSPORT6 vector  
 was constructed at Life Technologies, essentially  
 following the protocols of the SuperScript Plasmid System  
 full details of which are contained in the manufacturer's  
 instruction manual (http://www.lifetech.com/). First  
 strand synthesis was carried out using a Not I  
 primer-adaptor  
 [5'-PGACTAGTCTAGATCGGCGCGCC(T)15-3']. Not I/blunt  
 end inserts were cloned into the Not I/BcoR V sites in the  
 vector. EST analysis was performed on the unamplified  
 library at the NIH Intramural Sequencing Center (NISC)."

Query Match 56.0%; Score 610; DB 2; Length 636;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-294;  
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGGGGTCTCCACTCTCTGAGGTATTTTTCAGCCGCTGTCTCGCGCGCGCGGGGAG 120

Db 87 GGGGGTCTCCACTCTCTGAGGTATTTTTCAGCCGCTGTCTCGCGCGCGCGGGGAG 146

QY 121 CCGCGCTACATCGCGTGGAGTACGTACACACGCAATCTCGCGTTCGACAGCGAC 180

Db 147 CCGCGCTACATCGCGTGGAGTACGTACACACGCAATCTCGCGTTCGACAGCGAC 206

QY 181 GCGCGATTCCGAGGATGGAGCGCGGGAGCGCTGGGTGGAGCAAGAGGGCGCCAGTAT 240



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